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| (54) Title: <i>CHLAMYDIA TRACHOMATIS</i> GENOMIC SEQUENCE AND POLYPEPTIDES, FRAGMENTS THEREOF AND USES THEREOF, IN PARTICULAR FOR THE DIAGNOSIS, PREVENTION AND TREATMENT OF INFECTION (57) Abstract <p>The subject of the invention is the genomic sequence and the nucleotide sequences encoding polypeptides of <i>Chlamydia trachomatis</i>, such as cellular envelope polypeptides, which are secreted or specific, or which are involved in metabolism, in the replication process or in virulence, polypeptides encoded by such sequences, as well as vectors including the said sequences and cells or animals transformed with these vectors. The invention also relates to transcriptional gene products of the <i>Chlamydia trachomatis</i> genome, such as, for example, antisense and ribozyme molecules, which can be used to control growth of the microorganism. The invention also relates to methods of detecting these nucleic acids or polypeptides and kits for diagnosing <i>Chlamydia trachomatis</i> infection. The invention also relates to a method of selecting compounds capable of modulating bacterial infection and a method for the biosynthesis or biodegradation of molecules of interest using the said nucleotide sequences or the said polypeptides. The invention finally comprises, pharmaceutical, in particular vaccine, compositions for the prevention and/or treatment of bacterial, in particular <i>Chlamydia trachomatis</i>, infections.</p> | | |

The DNA sequence encoding the antigenic polypeptide and regulatory element may be inserted into a stable cell line or cloned microorganism, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described *e.g.*, in Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is incorporated herein by
5 reference in its entirety.

Such cell lines and microorganisms may be formulated for vaccine purposes. In yet another embodiment, the DNA sequence encoding the antigenic polypeptide and regulatory element may be delivered to a mammalian host and introduced into the host genome via homologous recombination (*See*, Chappel, U.S. Patent No. 4,215,051; Skoultchi, WO 91/06667 each of which is
10 incorporated herein by reference in its entirety.

Preferably, the immunogenic and/or vaccine compositions according to the invention intended for the prevention and/or the treatment of an infection by *Chlamydia pneumoniae* or by an associated microorganism will be chosen from the immunogenic and/or vaccine compositions comprising a polypeptide or one of its representative fragments corresponding to a protein, or one of
15 its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*. The vaccine compositions comprising nucleotide sequences will also preferably comprise nucleotide sequences encoding a polypeptide or one of its representative fragments corresponding to a protein, or one of its representative fragments, of the cellular envelope of *Chlamydia pneumoniae*.

Among these preferred immunogenic and/or vaccine compositions, the most preferred are
20 those comprising a polypeptide or one of its representative fragments, or a nucleotide sequence or one of its representative fragments whose sequences are chosen from the nucleotide or amino acid sequences identified in this functional group and listed above.

The polypeptides of the invention or their representative fragments entering into the immunogenic compositions according to the invention may be selected by techniques known to
25 persons skilled in the art, such as for example on the capacity of the said polypeptides to stimulate T cells, which results, for example, in their proliferation or the secretion of interleukins, and which leads to the production of antibodies directed against the said polypeptides.

In mice, in which a weight dose of the vaccine composition comparable to the dose used in humans is administered, the antibody reaction is tested by collecting serum followed by a study of
30 the formation of a complex between the antibodies present in the serum and the antigen of the vaccine composition, according to the customary techniques.

According to the invention, the said vaccine compositions will be preferably in combination with a pharmaceutically acceptable vehicle and, where appropriate, with one or more appropriate immunity adjuvants.

35 Various types of vaccines are currently available for protecting humans against infectious diseases: attenuated live microorganisms (*M. bovis* - BCG for tuberculosis), inactivated microorganisms (influenza virus), acellular extracts (*Bordetella pertussis* for whooping cough),

recombinant proteins (hepatitis B virus surface antigen), polysaccharides (pneumococci). Experiments are underway on vaccines prepared from synthetic peptides or from genetically modified microorganisms expressing heterologous antigens. Even more recently, recombinant plasmid DNAs carrying genes encoding protective antigens were proposed as an alternative vaccine strategy. This type of vaccination is carried out with a particular plasmid derived from an *E. coli* plasmid which does not replicate *in vivo* and which encodes only the vaccinal protein. Animals were immunized by simply injecting the naked plasmid DNA into the muscle. This technique leads to the expression of the vaccine protein *in situ* and to a cell-type (CTL) and a humoral type (antibody) immune response. This double induction of the immune response is one of the main advantages of the technique of vaccination with naked DNA.

The vaccine compositions of the present invention can be evaluated *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization assays such as those described by Peterson et al. (1988) can be utilized. The assay described by Peterson et al. (1988) is suitable for testing vaccine compositions directed toward either *Chlamydia pneumoniae* or *Chlamydia trachomatis*.

Briefly, hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydiae* (10^4 IFU; infectious units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37EC for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37E for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with a *Chlamydiae* specific antibody, such as anti-MOMP for *C. trachomatis*, etc. IFUs are counted in ten fields at a magnification of 200X. Neutralization titer is assigned based on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can be determined *in vivo* by challenging animal models of *Chlamydia pneumoniae* infection, e.g., mice or rabbits, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies can be performed in the murine model of *Chlamydia pneumoniae* infection described by Moazed et al. (1997). Briefly, male homozygous apoE deficient and/or C57 BL/6J mice are immunized with vaccine compositions. Post-vaccination, the mice are mildly sedated by subcutaneous injection of a mixture of ketamine and xylazine, and inoculated intranasally with a total volume of 0.03-0.05 ml of organisms suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/mouse. The mice are inoculated with *Chlamydia pneumoniae* at 8, 10, and 12 weeks of age. Tissues are then collected from the lung, spleen, heart, etc. at 1-20 weeks after the first inoculation. The presence of organisms is scored using PCR, histology and immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

Alternatively, *in vivo* vaccine composition challenge studies can be performed in the rabbit model of *Chlamydia pneumoniae* described by Laitinen et al. (1997). Briefly, New Zealand white rabbits (5 months old) are immunized with the vaccine compositions. Post-vaccination, the rabbits are sedated with Hypnorm, 0.3 ml/Kg of body weight, intramuscularly, and inoculated
5 intranasally with a total of 0.5 ml of *Chlamydia pneumoniae* suspended in SPG medium or with SPG alone. The inoculations of *Chlamydia pneumoniae* are approximately 3×10^7 IFU/rabbit. The rabbits are reinfected in the same manner and with the same dose 3 weeks after the primary inoculation. Tissues are then collected 2 weeks after the primary infection and 1, 2, and 4 weeks after the reinfection. The presence of *Chlamydia pneumoniae* is scored using PCR, histology and
10 immunocytochemistry, or by quantitative culture/IFU after tissue homogenization.

The vaccine compositions comprising nucleotide sequences or vectors into which the said sequences are inserted are in particular described in International Application No. WO 90/11092 and also in International Application No. WO 95/11307.

The nucleotide sequence constituting the vaccine composition according to the invention
15 may be injected into the host after having been coupled to compounds which promote the penetration of this polynucleotide inside the cell or its transport up to the cell nucleus. The resulting conjugates may be encapsulated into polymeric microparticles, as described in International Application No. WO 94/27238 (Medisorb Technologies International).

According to another embodiment of the vaccine composition according to the invention,
20 the nucleotide sequence, preferably a DNA, is complexed with the DEAE-dextran (Pagano et al., 1967) or with nuclear proteins (Kaneda et al., 1989), with lipids (Felgner et al., 1987) or encapsulated into liposomes (Fraley et al., 1980) or alternatively introduced in the form of a gel facilitating its transfection into the cells (Midoux et al., 1993, Pastore et al., 1994). The polynucleotide or the vector according to the invention may also be in suspension in a buffer solution or may be combined with
25 liposomes.

Advantageously, such a vaccine will be prepared in accordance with the technique described by Tacson et al. or Huygen et al. in 1996 or alternatively in accordance with the technique described by Davis et al. in International Application No. WO 95/11307.

Such a vaccine may also be prepared in the form of a composition containing a vector
30 according to the invention, placed under the control of regulatory elements allowing its expression in humans or animals. It is possible, for example, to use, as vector for the *in vivo* expression of the polypeptide antigen of interest, the plasmid pcDNA3 or the plasmid pcDNA1/neo, both marketed by Invitrogen ® & D Systems, Abingdon, United Kingdom). It is also possible to use the plasmid V1Jns.tPA, described by Shiver et al. in 1995. Such a vaccine will advantageously comprise, in
35 addition to the recombinant vector, a saline solution, for example a sodium chloride solution.

The immunogenic compositions of the invention can also be utilized as part of methods for immunization, wherein such methods comprise administering to a host, e.g., a human host, an

immunizing amount of the immunogenic compositions of the invention. In a preferred embodiment, the method of immunizing is a method of immunizing against *Chlamydia pneumoniae*.

A pharmaceutically acceptable vehicle is understood to designate a compound or a combination of compounds entering into a pharmaceutical or vaccine composition which does not
5 cause side effects and which makes it possible, for example, to facilitate the administration of the active compound, to increase its life and/or its efficacy in the body, to increase its solubility in solution or alternatively to enhance its preservation. These pharmaceutically acceptable vehicles are well known and will be adapted by persons skilled in the art according to the nature and the mode of administration of the active compound chosen.

10 As regards the vaccine formulations, these may comprise appropriate immunity adjuvants which are known to persons skilled in the art, such as, for example, aluminum hydroxide, a representative of the family of muramyl peptides such as one of the peptide derivatives of N-acetyl-muramyl, a bacterial lysate, or alternatively incomplete Freund's adjuvant, Stimulon™ QS-21 (Aquila Biopharmaceuticals, Inc., Framingham, MA), MPL™ (3-O-deacylated monophosphoryl lipid A; RIBI
15 ImmunoChem Research, Inc., Hamilton, MT), aluminum phosphate, IL-12 (Genetics Institute, Cambridge, MA).

Preferably, these compounds will be administered by the systemic route, in particular by the intravenous route, by the intranasal, intramuscular, intradermal or subcutaneous route, or by the oral route. More preferably, the vaccine composition comprising polypeptides according to the
20 invention will be administered several times, spread out over time, by the intradermal or subcutaneous route.

Their optimum modes of administration, dosages and galenic forms may be determined according to criteria which are generally taken into account in establishing a treatment adapted to a patient, such as for example the patient's age or body weight, the seriousness of his general condition,
25 tolerance of the treatment and the side effects observed.

The invention comprises the use of a composition according to the invention for the treatment or the prevention of cardiovascular diseases, preferably linked to the presence of atheroma, which are induced or worsened by *Chlamydia pneumoniae*.

Finally, the invention comprises the use of a composition according to the invention for
30 the treatment or the prevention of respiratory diseases which are induced or worsened by the presence of *Chlamydia pneumoniae*, preferably asthma.

Other characteristics and advantages of the invention appear in the following examples and figures:

35 Legend to the figures :

Figure 1 : Line for the production of *Chlamydia pneumoniae* sequences

| TABLE 1 | | | | | | | Score | I% |
|---------|-------|-------|--|--------|------------------------------|--|-------|----|
| ORF | Begin | End | Homology | ID | Species | | | |
| ORF2 | 42 | 794 | triosephosphate isomerase | L27492 | <i>Thermotoga maritima</i> | | 567 | 54 |
| ORF3 | 1258 | 1614 | putative | | | | | |
| ORF4 | 1807 | 2418 | polypeptide deformylase | D90906 | <i>Synechocystis sp.</i> | | 316 | 40 |
| ORF5 | 3393 | 2491 | hypothetical protein | Z75208 | <i>Bacillus subtilis</i> | | 338 | 42 |
| ORF6 | 3639 | 4067 | unknown | U87792 | <i>Bacillus subtilis</i> | | 117 | 38 |
| ORF7 | 5649 | 4270 | putative | | | | | |
| ORF8 | 7463 | 6012 | putative | | | | | |
| ORF9 | 8051 | 8962 | putative | | | | | |
| ORF10 | 9129 | 9959 | putative | | | | | |
| ORF11 | 10687 | 10361 | putative | | | | | |
| ORF12 | 10927 | 11232 | putative | | | | | |
| ORF13 | 11246 | 12727 | amidase | U49269 | <i>Moraxella catarrhalis</i> | | 1108 | 42 |
| ORF14 | 12691 | 14190 | PET112 | D90913 | <i>Synechocystis sp.</i> | | 1044 | 46 |
| ORF15 | 14484 | 17249 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | | 1074 | 43 |
| ORF16 | 16039 | 15770 | putative | | | | | |
| ORF17 | 17845 | 20853 | putative | | | | | |
| ORF18 | 21137 | 22042 | putative | | | | | |
| ORF19 | 22046 | 23476 | putative | | | | | |
| ORF20 | 23681 | 26110 | putative | | | | | |
| ORF21 | 26109 | 25861 | putative | | | | | |
| ORF22 | 26241 | 26978 | putative | | | | | |
| ORF23 | 26960 | 27754 | putative | | | | | |
| ORF24 | 27747 | 28577 | putative | | | | | |
| ORF25 | 28887 | 29492 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | | 180 | 39 |
| ORF26 | 29432 | 30028 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | | 361 | 51 |
| ORF27 | 30024 | 31472 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | | 879 | 54 |
| ORF28 | 31758 | 32288 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | | 144 | 43 |
| ORF29 | 32201 | 33991 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | | 1126 | 48 |
| ORF30 | 33852 | 34541 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | | 589 | 62 |
| ORF31 | 34783 | 36063 | POMP91B precursor | U65943 | <i>Chlamydia psittaci</i> | | 469 | 46 |
| ORF32 | 36009 | 37529 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | | 1338 | 51 |
| ORF33 | 37881 | 39362 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | | 671 | 40 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|-------|-------|-------|--|----------|----------------------------------|-------|----|
| ORF34 | 39418 | 39161 | putative | | | | |
| ORF35 | 39366 | 40715 | POMP90A precursor | U65942 | <i>Chlamydia psittaci</i> | 904 | 47 |
| ORF36 | 43076 | 41094 | putative | | | | |
| ORF37 | 43800 | 43066 | putative | | | | |
| ORF38 | 44828 | 43785 | putative | | | | |
| ORF39 | 45340 | 44753 | homologous to unidentified E. coli protein | M96343 | <i>Bacillus subtilis</i> | 136 | 44 |
| ORF40 | 45752 | 45372 | o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHES HAEIN SW: P44808 | AE000184 | <i>Escherichia coli</i> | 269 | 43 |
| ORF41 | 46996 | 45701 | ABC transporter, ATP-binding protein (yheS) | AE000596 | <i>Helicobacter pylori</i> | 878 | 39 |
| ORF42 | 47961 | 47569 | putative | | | | |
| ORF43 | 48960 | 48040 | hypothetical protein | D64001 | <i>Synechocystis</i> sp. | 404 | 37 |
| ORF44 | 51452 | 50133 | Lon protease-like protein | X74215 | <i>Homo sapiens</i> | 1232 | 54 |
| ORF45 | 52606 | 51335 | unknown | Z54285 | <i>Schizosaccharomyces pombe</i> | 781 | 47 |
| ORF46 | 53684 | 53319 | putative | | | | |
| ORF47 | 54195 | 53746 | putative | | | | |
| ORF48 | 55278 | 56453 | heat-shock protein | U15010 | <i>Legionella pneumophila</i> | 975 | 45 |
| ORF49 | 56493 | 57266 | branched chain alpha-keto acid dehydrogenase E1-alpha | M97391 | <i>Bacillus subtilis</i> | 329 | 36 |
| ORF50 | 57297 | 58526 | branched chain alpha-keto acid dehydrogenase E1-beta | M97391 | <i>Bacillus subtilis</i> | 707 | 50 |
| ORF51 | 59851 | 58565 | putative | | | | |
| ORF52 | 61495 | 59924 | ComE | D90903 | <i>Synechocystis</i> sp. | 134 | 55 |
| ORF53 | 61324 | 62151 | putative | | | | |
| ORF54 | 62132 | 62470 | Hpr protein | X12832 | <i>Bacillus subtilis</i> | 136 | 36 |
| ORF55 | 62474 | 63733 | enzyme I (ptsI) | U32844 | <i>Haemophilus influenzae</i> | 381 | 35 |
| ORF56 | 63881 | 64186 | f831; This 831 aa orf is 46 pct identical (11 gaps) to 709 residues of an approx. 712 aa protein PT1A ECOLI SW: P32670 | AE000326 | <i>Escherichia coli</i> | 123 | 34 |
| ORF57 | 64611 | 64318 | ORF107 | X17014 | <i>Bacillus subtilis</i> | 128 | 33 |
| ORF58 | 65485 | 64673 | putative | | | | |
| ORF59 | 65999 | 65301 | dnaZX-like ORF put. DNA polymerase III | X06803 | <i>Bacillus subtilis</i> | 596 | 52 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|-------|--------|--------|--|----------|-------------------------------|-------|----|
| ORF60 | 66244 | 67281 | putative | | | | |
| ORF61 | 67265 | 67699 | putative | | | | |
| ORF62 | 67703 | 68539 | putative | | | | |
| ORF63 | 68805 | 70736 | putative | | | | |
| ORF64 | 69172 | 68831 | putative | | | | |
| ORF65 | 70642 | 71142 | putative | | | | |
| ORF66 | 71325 | 72029 | putative | | | | |
| ORF67 | 72060 | 73637 | putative | | | | |
| ORF68 | 74061 | 76175 | YqfF | D84432 | <i>Bacillus subtilis</i> | 542 | 44 |
| ORF69 | 78351 | 77680 | porphobilinogen deaminase | D28503 | <i>Clostridium josui</i> | 262 | 42 |
| ORF70 | 79356 | 78355 | sms protein | D90914 | <i>Synechocystis</i> sp. | 736 | 52 |
| ORF71 | 79983 | 79693 | ribonuclease III (mc) | AE000579 | <i>Helicobacter pylori</i> | 98 | 33 |
| ORF72 | 80441 | 79938 | ORF3 | D64116 | <i>Bacillus subtilis</i> | 268 | 44 |
| ORF73 | 80475 | 80969 | putative | | | | |
| ORF74 | 81296 | 83080 | hypothetical protein | Y14079 | <i>Bacillus subtilis</i> | 893 | 38 |
| ORF75 | 83291 | 83932 | manganese superoxide dismutase | X77021 | <i>Caenorhabditis elegans</i> | 622 | 58 |
| ORF76 | 84005 | 84769 | acetyl-CoA carboxylase beta subunit (accD) | AE000604 | <i>Helicobacter pylori</i> | 602 | 50 |
| ORF77 | 84975 | 85244 | deoxyuridinetriphosphatase (dut) | U32776 | <i>Haemophilus influenzae</i> | 110 | 41 |
| ORF78 | 85123 | 85425 | deoxyuridine 5'-triphosphate nucleotidohydrolase (dut) | AE000596 | <i>Helicobacter pylori</i> | 265 | 68 |
| ORF79 | 85397 | 85903 | ORF2 | L26916 | <i>Pseudomonas aeruginosa</i> | 173 | 34 |
| ORF80 | 85909 | 86583 | enzyme IIANtr | U18997 | <i>Escherichia coli</i> | 170 | 42 |
| ORF81 | 86626 | 88065 | putative | | | | |
| ORF82 | 89257 | 91026 | putative | | | | |
| ORF83 | 91291 | 93030 | putative | | | | |
| ORF84 | 93295 | 94086 | putative | | | | |
| ORF85 | 95285 | 94707 | putative | | | | |
| ORF86 | 95667 | 96557 | putative | | | | |
| ORF87 | 96317 | 97456 | putative | | | | |
| ORF88 | 98435 | 97968 | putative | | | | |
| ORF89 | 99460 | 98426 | putative | | | | |
| ORF90 | 100144 | 101325 | elongation factor Tu | L22216 | <i>Chlamydia trachomatis</i> | 1917 | 95 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|---------------------------------------|-------|----|
| ORF91 | 101457 | 101720 | putative | | | | |
| ORF92 | 101704 | 102273 | transcription factor | L10348 | <i>Thermus aquaticus thermophilus</i> | 376 | 49 |
| ORF93 | 102356 | 102805 | ribosomal protein L11 | D13303 | <i>Bacillus subtilis</i> | 458 | 63 |
| ORF94 | 102835 | 103530 | ribosomal protein L1 | Z11839 | <i>Thermotoga maritima</i> | 642 | 51 |
| ORF95 | 103549 | 104058 | ribosomal protein L10 | M89911 | <i>Streptomyces antibioticus</i> | 82 | 31 |
| ORF96 | 104096 | 104491 | rp12 (AA 1-128) | X53178 | <i>Synechocystis PCC6803</i> | 325 | 47 |
| ORF97 | 104601 | 108386 | DNA-directed RNA polymerase beta chain | X64172 | <i>Staphylococcus aureus</i> | 2740 | 52 |
| ORF98 | 108401 | 112054 | rpoC | V00339 | <i>Escherichia coli</i> | 2947 | 54 |
| ORF99 | 112033 | 112590 | acetylornithine deacetylase (EC 5.1.1.16) | M22622 | <i>Leptospira biflexa</i> | 514 | 62 |
| ORF100 | 112672 | 113682 | transaldolase | L19437 | <i>Homo sapiens</i> | 755 | 49 |
| ORF101 | 113726 | 114121 | putative | | | | |
| ORF102 | 114711 | 114136 | putative | | | | |
| ORF103 | 115267 | 115755 | putative | | | | |
| ORF104 | 115911 | 116543 | putative | | | | |
| ORF105 | 116736 | 118055 | ATPase alpha-subunit | X63855 | <i>Thermus aquaticus thermophilus</i> | 934 | 50 |
| ORF106 | 117968 | 118522 | adenosine triphosphatase A subunit | D50528 | <i>Acetabularia acetabulum</i> | 147 | 32 |
| ORF107 | 118530 | 119843 | V-ATPase B subunit | U96487 | <i>Desulfurococcus sp. SY</i> | 751 | 48 |
| ORF108 | 119816 | 120457 | putative | | | | |
| ORF109 | 120451 | 122430 | v-type Na-ATPase | X76913 | <i>Enterococcus hirae</i> | 264 | 35 |
| ORF110 | 122504 | 122950 | ATP synthase, subunit K | U67478 | <i>Methanococcus jannaschii</i> | 184 | 31 |
| ORF111 | 123528 | 126347 | valyl-tRNA synthetase | X05891 | <i>Escherichia coli</i> | 1679 | 49 |
| ORF112 | 126332 | 129166 | protein kinase-like protein | U19250 | <i>Streptomyces coelicolor</i> | 427 | 37 |
| ORF113 | 134690 | 129213 | UvrA | D49911 | <i>Thermus thermophilus</i> | 3107 | 41 |
| ORF114 | 134925 | 136382 | pyruvate kinase | U83196 | <i>Chlamydia trachomatis</i> | 1748 | 71 |
| ORF115 | 137870 | 136482 | HtrB protein | X61000 | <i>Escherichia coli</i> | 147 | 38 |
| ORF116 | 137899 | 138240 | putative | | | | |
| ORF117 | 138239 | 137928 | putative | | | | |
| ORF118 | 139558 | 138257 | putative | | | | |
| ORF119 | 140352 | 139516 | YbbP | AB002150 | <i>Bacillus subtilis</i> | 231 | 46 |
| ORF120 | 140498 | 141841 | cyanide insensitive terminal oxidase | Y10528 | <i>Pseudomonas aeruginosa</i> | 538 | 50 |
| ORF121 | 141855 | 142658 | cyanide insensitive terminal oxidase | Y10528 | <i>Pseudomonas aeruginosa</i> | 310 | 40 |
| ORF122 | 144258 | 143050 | putative | | | | |
| ORF123 | 145258 | 144494 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | % |
|--------|--------|--------|---|----------|----------------------------------|-------|----|
| ORF124 | 145454 | 146749 | product similar to E. coli PhoH protein | Z97025 | <i>Bacillus subtilis</i> | 836 | 47 |
| ORF125 | 147318 | 146767 | putative | | | | |
| ORF126 | 148261 | 147677 | putative | | | | |
| ORF127 | 149029 | 152157 | isoleucyl-tRNA synthetase | U04953 | <i>Homo sapiens</i> | 2361 | 52 |
| ORF128 | 154108 | 152201 | leader peptidase I | D90904 | <i>Synechocystis sp.</i> | 225 | 47 |
| ORF129 | 155135 | 154308 | putative | | | | |
| ORF130 | 155141 | 155467 | YtiA | AF008220 | <i>Bacillus subtilis</i> | 201 | 43 |
| ORF131 | 155703 | 156779 | orf 361; translated orf similarity to SW: RF1_SALTY peptide chain release factor 1 of <i>Salmonella typhimurium</i> | X78969 | <i>Coxiella burnetii</i> | 863 | 59 |
| ORF132 | 156748 | 157635 | product similar to E. coli PRFA2 protein | Z49782 | <i>Bacillus subtilis</i> | 144 | 37 |
| ORF133 | 157653 | 158996 | Ffh | U82109 | <i>Thermus aquaticus</i> | 797 | 45 |
| ORF134 | 159363 | 159986 | tRNA (guanine-N1)-methyltransferase (trmD) | U32705 | <i>Haemophilus influenzae</i> | 545 | 49 |
| ORF135 | 159880 | 160446 | putative | | | | |
| ORF136 | 160477 | 160839 | ribosomal protein L19 | X72627 | <i>Synechocystis sp.</i> | 319 | 50 |
| ORF137 | 160898 | 161539 | putative protein highly homologous to E. coli RNase HIII. | D32253 | <i>Magnetospirillum sp.</i> | 427 | 49 |
| ORF138 | 161527 | 162153 | 5'guanylate kinase (gmk) | U32848 | <i>Haemophilus influenzae</i> | 385 | 43 |
| ORF139 | 162144 | 162443 | putative | | | | |
| ORF140 | 162437 | 164098 | methionyl-tRNA synthetase | AB004537 | <i>Schizosaccharomyces pombe</i> | 861 | 54 |
| ORF141 | 165451 | 164228 | exodeoxyribonuclease V (recD) | U32811 | <i>Haemophilus influenzae</i> | 432 | 32 |
| ORF142 | 166349 | 165411 | putative | | | | |
| ORF143 | 166949 | 168442 | putative | | | | |
| ORF144 | 169416 | 171029 | putative | | | | |
| ORF145 | 170857 | 171459 | putative | | | | |
| ORF146 | 172652 | 173428 | putative biotin-protein ligase | Z97992 | <i>Schizosaccharomyces pombe</i> | 292 | 44 |
| ORF147 | 174626 | 173439 | putative | | | | |
| ORF148 | 174816 | 175613 | putative | | | | |
| ORF149 | 175598 | 175954 | putative | | | | |
| ORF150 | 175958 | 176935 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|-------------------------------------|-------|-----|
| ORF151 | 177708 | 176938 | orf 3' of chaperonin homolog hypB [Chlamydia psittaci, pigeon strain P-1041, Pentide Partial, 98 aa] | S40172 | <i>Chlamydia psittaci</i> | 376 | 74 |
| ORF152 | 177128 | 177376 | putative | | | | |
| ORF153 | 179472 | 177841 | putative | M69217 | <i>Chlamydia pneumoniae</i> | 2678 | 100 |
| ORF154 | 179822 | 179517 | putative | M69217 | <i>Chlamydia pneumoniae</i> | 498 | 99 |
| ORF155 | 181793 | 179943 | Pz-peptidase | D88209 | <i>Bacillus licheniformis</i> | 1088 | 38 |
| ORF156 | 182628 | 181876 | o247; This 247 aa orf is 51 pct identical (0 gaps) to 117 residues of an approx. 160 aa protein YPH7_CHRV1SW.P45371 | AE000174 | <i>Escherichia coli</i> | 401 | 42 |
| ORF157 | 184420 | 183074 | glutamate-1-semialdehyde 2,1- aminomutase | X53696 | <i>Escherichia coli</i> | 823 | 41 |
| ORF158 | 184988 | 184467 | ORF o211 | U28377 | <i>Escherichia coli</i> | 87 | 54 |
| ORF159 | 185483 | 185112 | hypothetical protein | D90906 | <i>Synechocystis</i> sp. | 91 | 33 |
| ORF160 | 185902 | 185483 | ribose 5-phosphate isomerase | U28377 | <i>Escherichia coli</i> | 111 | 41 |
| ORF161 | 186174 | 185839 | ribose 5-phosphate isomerase A (SP:P27252) | U32729 | <i>Haemophilus influenzae</i> | 190 | 46 |
| ORF162 | 187720 | 186587 | hypothetical | D83026 | <i>Bacillus subtilis</i> | 536 | 42 |
| ORF163 | 188318 | 190933 | ATP-dependent protease binding subunit | M29364 | <i>Escherichia coli</i> | 2010 | 53 |
| ORF164 | 191090 | 191635 | putative | | | | |
| ORF165 | 191547 | 192743 | putative | | | | |
| ORF166 | 192969 | 193469 | putative | | | | |
| ORF167 | 194044 | 193610 | putative | | | | |
| ORF168 | 194196 | 195809 | unknown | Z84395 | <i>Mycobacterium tuberculosis</i> | 242 | 52 |
| ORF169 | 196088 | 198073 | DNA ligase (EC 6.5.1.2) | M24278 | <i>Escherichia coli</i> | 1317 | 46 |
| ORF170 | 198132 | 199454 | putative | | | | |
| ORF171 | 199351 | 202818 | putative | | | | |
| ORF172 | 204552 | 202999 | PcpB | U60175 | <i>Sphingomonas chlorophenolica</i> | 80 | 41 |
| ORF173 | 205648 | 204692 | putative | | | | |
| ORF174 | 205807 | 207327 | leucine tRNA synthetase | AF008220 | <i>Bacillus subtilis</i> | 1595 | 57 |
| ORF175 | 207182 | 207775 | leucyl-tRNA synthetase | X06331 | <i>Escherichia coli</i> | 363 | 51 |
| ORF176 | 207779 | 208267 | transfer RNA-Leu synthetase | M88581 | <i>Bacillus subtilis</i> | 285 | 43 |
| ORF177 | 208267 | 209577 | KDO transferase | Z31593 | <i>Chlamydia pneumoniae</i> | 2262 | 100 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|--------|------------------------------------|-------|----|
| ORF178 | 211807 | 211271 | KDO-transferase | X80061 | <i>Chlamydia psittaci</i> | 105 | 38 |
| ORF179 | 212188 | 211844 | putative | | | | |
| ORF180 | 214079 | 212448 | pyrophosphate-dependent phosphofructokinase beta subunit | Z32850 | <i>Ricinus communis</i> | 1003 | 45 |
| ORF181 | 214907 | 214083 | CinI | U44893 | <i>Butyrivibrio fibrisolvens</i> | 111 | 41 |
| ORF182 | 216154 | 215429 | putative | | | | |
| ORF183 | 216115 | 216678 | putative | | | | |
| ORF184 | 216728 | 217282 | putative | | | | |
| ORF185 | 217267 | 217866 | putative | | | | |
| ORF186 | 218593 | 218261 | putative | | | | |
| ORF187 | 219821 | 218994 | putative | | | | |
| ORF188 | 221382 | 220309 | putative | | | | |
| ORF189 | 222719 | 221433 | GMP synthetase | M10101 | <i>Escherichia coli</i> | 1151 | 48 |
| ORF190 | 223521 | 222724 | IMP dehydrogenase | X66859 | <i>Acinetobacter calcoaceticus</i> | 778 | 58 |
| ORF191 | 224499 | 225008 | putative | | | | |
| ORF192 | 225140 | 225559 | putative | | | | |
| ORF193 | 225555 | 226802 | putative | | | | |
| ORF194 | 227800 | 226892 | putative | | | | |
| ORF195 | 228335 | 228072 | putative | | | | |
| ORF196 | 229251 | 228643 | putative | | | | |
| ORF197 | 230983 | 229622 | YqhX | D84432 | <i>Bacillus subtilis</i> | 1386 | 56 |
| ORF198 | 231483 | 230983 | acetyl-CoA carboxylase biotin carboxyl carrier protein | U38804 | <i>Porphyra purpurea</i> | 199 | 52 |
| ORF199 | 232063 | 231509 | elongation factor P | D64001 | <i>Synechocystis sp.</i> | 282 | 32 |
| ORF200 | 232739 | 232053 | pentose-5-phosphate-3-epimerase | D90911 | <i>Synechocystis sp.</i> | 463 | 43 |
| ORF201 | 233166 | 234356 | putative | | | | |
| ORF202 | 233518 | 233165 | putative | | | | |
| ORF203 | 234536 | 235186 | ORF2 | L35036 | <i>Chlamydia psittaci</i> | 570 | 60 |
| ORF204 | 235379 | 236689 | putative | | | | |
| ORF205 | 236680 | 237618 | putative | | | | |
| ORF206 | 237521 | 238345 | putative | | | | |
| ORF207 | 238281 | 238973 | putative | | | | |
| ORF208 | 238871 | 240115 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|--------------------------------|-------|----|
| ORF209 | 240191 | 241564 | putative | | | | |
| ORF210 | 242281 | 241604 | YqJZ | D84432 | <i>Bacillus subtilis</i> | 379 | 39 |
| ORF211 | 242933 | 242274 | F222; This 222 aa orf is 48 pct identical (0 gaps) to 208 residues of an approx. 232 aa protein YCKA BACSU SW: P42399 | AE000284 | <i>Escherichia coli</i> | 382 | 45 |
| ORF212 | 243416 | 242976 | arginine repressor protein (argR) | U32800 | <i>Haemophilus influenzae</i> | 229 | 46 |
| ORF213 | 243500 | 244531 | sialoglycoprotease | U15958 | <i>Pasteurella haemolytica</i> | 565 | 53 |
| ORF214 | 244480 | 246021 | oligopeptide permease homolog AII | AF000366 | <i>Borrelia burgdorferi</i> | 457 | 34 |
| ORF215 | 246330 | 247811 | OppAIV | AF000948 | <i>Borrelia burgdorferi</i> | 453 | 35 |
| ORF216 | 247831 | 249174 | OppA gene product | X56347 | <i>Bacillus subtilis</i> | 255 | 37 |
| ORF217 | 249437 | 251038 | deiAE | X56678 | <i>Bacillus subtilis</i> | 469 | 37 |
| ORF218 | 251325 | 252212 | OppB gene product | X56347 | <i>Bacillus subtilis</i> | 652 | 42 |
| ORF219 | 253156 | 254007 | oligopeptidase | X89237 | <i>Streptococcus pyogenes</i> | 574 | 48 |
| ORF220 | 253974 | 254852 | ATP binding protein | L18760 | <i>Lactococcus lactis</i> | 433 | 40 |
| ORF221 | 255258 | 256094 | KDO-transferase | X80061 | <i>Chlamydia psittaci</i> | 106 | 46 |
| ORF222 | 256640 | 257455 | putative | | | | |
| ORF223 | 257502 | 258239 | 2-OXOGLUTARAT | A47930 | <i>Spinacia oleracea</i> | 636 | 52 |
| ORF224 | 257869 | 257501 | putative | | | | |
| ORF225 | 259248 | 260897 | pyrophosphate-fructose 6-phosphate 1-phosphotransferase beta-subunit | M55191 | <i>Solanum tuberosum</i> | 1055 | 44 |
| ORF226 | 262753 | 261788 | putative | | | | |
| ORF227 | 263059 | 262757 | putative | | | | |
| ORF228 | 264375 | 263182 | putative | | | | |
| ORF229 | 265985 | 264747 | putative | | | | |
| ORF230 | 266637 | 266059 | putative | | | | |
| ORF231 | 267338 | 266538 | putative | | | | |
| ORF232 | 267922 | 267473 | putative | | | | |
| ORF233 | 269647 | 270771 | tRNA guanine transglycosylase | L33777 | <i>Zymomonas mobilis</i> | 628 | 44 |
| ORF234 | 272777 | 273145 | ORF 4 | D00624 | <i>Bacteriophage phi1</i> | 100 | 41 |
| ORF235 | 273253 | 273636 | putative | | | | |
| ORF236 | 273705 | 273977 | putative | | | | |
| ORF237 | 276016 | 275717 | putative | | | | |
| ORF238 | 276439 | 276020 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | 1% |
|--------|--------|--------|--|----------|---|-------|----|
| ORF239 | 276792 | 277253 | putative | | | | |
| ORF240 | 277318 | 277599 | putative | | | | |
| ORF241 | 278578 | 277877 | putative | | | | |
| ORF242 | 279258 | 278554 | FbpC | U33937 | <i>Neisseria gonorrhoeae</i> | 312 | 39 |
| ORF243 | 280435 | 279533 | putative | | | | |
| ORF244 | 281547 | 280849 | putative | | | | |
| ORF245 | 281696 | 282325 | CMP-2-keto-3-deoxyoctulosonic acid synthetase | U15192 | <i>Chlamydia trachomatis</i> | 637 | 63 |
| ORF246 | 282459 | 284069 | CTP synthetase | U15192 | <i>Chlamydia trachomatis</i> | 2000 | 68 |
| ORF247 | 284056 | 284517 | ORF3 | U15192 | <i>Chlamydia trachomatis</i> | 453 | 65 |
| ORF248 | 284606 | 285775 | glucose 6-phosphate dehydrogenase | U83195 | <i>Chlamydia trachomatis</i> | 1263 | 77 |
| ORF249 | 285592 | 285987 | glucose 6-phosphate dehydrogenase | U83195 | <i>Chlamydia trachomatis</i> | 519 | 79 |
| ORF250 | 286179 | 286976 | glucose-6-phosphate dehydrogenase isozyme | D88189 | <i>Actinobacillus actinomycetemcomitans</i> | 216 | 40 |
| ORF251 | 287583 | 287002 | putative | | | | |
| ORF252 | 287951 | 287451 | putative | | | | |
| ORF253 | 288499 | 28816 | putative | | | | |
| ORF254 | 289674 | 288505 | putative | | | | |
| ORF255 | 288839 | 289213 | putative | | | | |
| ORF256 | 289970 | 290254 | putative | | | | |
| ORF257 | 291931 | 292803 | gamma-D-glutamyl-L-diamino acid endopeptidase II | X64809 | <i>Bacillus sphaericus</i> | 95 | 39 |
| ORF258 | 293258 | 292755 | ScoS9 | U43429 | <i>Streptomyces coelicolor</i> | 233 | 45 |
| ORF259 | 293718 | 293272 | ribosomal protein L13 (rpL13) | U32823 | <i>Haemophilus influenzae</i> | 364 | 47 |
| ORF260 | 294630 | 293953 | glutamine transport ATP-binding protein Q | U67524 | <i>Methanococcus jannaschii</i> | 387 | 46 |
| ORF261 | 296153 | 294636 | putative | | | | |
| ORF262 | 294817 | 295068 | putative | | | | |
| ORF263 | 296354 | 297862 | conserved hypothetical protein | AE000586 | <i>Helicobacter pylori</i> | 641 | 46 |
| ORF264 | 298415 | 297879 | putative | | | | |
| ORF265 | 298777 | 298253 | putative | | | | |
| ORF266 | 299572 | 298781 | putative | | | | |
| ORF267 | 300487 | 299633 | putative | | | | |
| ORF268 | 301586 | 300702 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|-----------------------------------|-------|----|
| ORF269 | 302440 | 301571 | putative | | | | |
| ORF270 | 302838 | 302437 | putative | | | | |
| ORF271 | 303335 | 302745 | putative | | | | |
| ORF272 | 304394 | 303852 | putative | | | | |
| ORF273 | 304606 | 305223 | f311; This 311 aa orf is 22 pct identical (13 gaps) to 186 residues of an approx. 488 aa protein YACA_BACSU SW: P37563; pyul of D21139 | AE000232 | <i>Escherichia coli</i> | 250 | 38 |
| ORF274 | 305394 | 306236 | survival protein surE | U81296 | <i>Sinorhizobium meliloti</i> | 156 | 42 |
| ORF275 | 306501 | 307439 | YqfU | D84432 | <i>Bacillus subtilis</i> | 547 | 42 |
| ORF276 | 308033 | 307458 | 3-octaprenyl-4-hydroxybenzoate carboxylase | U61168 | <i>Bacillus firmus</i> | 403 | 42 |
| ORF277 | 308924 | 308037 | 4-hydroxybenzoate octaprenyltransferase | U61168 | <i>Bacillus firmus</i> | 152 | 40 |
| ORF278 | 309485 | 310180 | putative | | | | |
| ORF279 | 310426 | 311214 | putative | | | | |
| ORF280 | 311597 | 311253 | putative | | | | |
| ORF281 | 312772 | 311780 | putative | | | | |
| ORF282 | 313425 | 312772 | putative | | | | |
| ORF283 | 313646 | 313377 | putative | | | | |
| ORF284 | 313937 | 314665 | lysophospholipase homolog | AF006678 | <i>Schistosoma mansoni</i> | 141 | 44 |
| ORF285 | 315576 | 314755 | dnaZX | X17014 | <i>Bacillus subtilis</i> | 154 | 39 |
| ORF286 | 316157 | 315531 | unknown | D26185 | <i>Bacillus subtilis</i> | 284 | 31 |
| ORF287 | 318657 | 316156 | DNA gyrase | L47978 | <i>Aeromonas salmonicida</i> | 1785 | 48 |
| ORF288 | 321042 | 318676 | DNA gyrase subunit B | U35453 | <i>Clostridium acetobutylicum</i> | 1838 | 59 |
| ORF289 | 321445 | 321098 | putative | | | | |
| ORF290 | 322309 | 321710 | putative | | | | |
| ORF291 | 323190 | 322366 | outer membrane protein | AE000654 | <i>Helicobacter pylori</i> | 376 | 43 |
| ORF292 | 323843 | 323181 | hypothetical | U70214 | <i>Escherichia coli</i> | 356 | 37 |
| ORF293 | 324878 | 323856 | ATP-binding protein (abc) | U32744 | <i>Haemophilus influenzae</i> | 545 | 44 |
| ORF294 | 325340 | 326410 | f374; This 374 aa orf is 30 pct identical (9 gaps) to 102 residues of an approx. 512 aa protein FLIC_SALMU SW: P06177 | AE000299 | <i>Escherichia coli</i> | 1194 | 62 |
| ORF295 | 326433 | 327836 | Xas A | AE000246 | <i>Escherichia coli</i> | 479 | 33 |

| ORF | Begin | End | Homology | ID | Species | Score | 1% |
|--------|--------|--------|---|----------|-------------------------------|-------|----|
| ORF296 | 328465 | 327839 | putative | | | | |
| ORF297 | 329360 | 328857 | putative | | | | |
| ORF298 | 330907 | 329357 | putative | | | | |
| ORF299 | 332455 | 330956 | MgE | U18744 | <i>Bacillus firmus</i> | 203 | 36 |
| ORF300 | 334536 | 332395 | putative | | | | |
| ORF301 | 336091 | 334877 | putative | | | | |
| ORF302 | 336103 | 337302 | putative | | | | |
| ORF303 | 338129 | 338830 | putative | | | | |
| ORF304 | 338965 | 339501 | putative | | | | |
| ORF305 | 339508 | 340143 | putative | | | | |
| ORF306 | 340247 | 342967 | putative | | | | |
| ORF307 | 343385 | 343810 | cAMP-dependent protein kinase type I regulatory subunit | U75932 | <i>Rattus norvegicus</i> | 102 | 37 |
| ORF308 | 344171 | 343935 | acyl carrier protein (acpP) | AE000570 | <i>Helicobacter pylori</i> | 198 | 55 |
| ORF309 | 345082 | 344330 | 3-ketoacyl-ACP reductase | U39441 | <i>Vibrio harveyi</i> | 598 | 48 |
| ORF310 | 346005 | 345082 | malonyl-CoA:Acyl carrier protein transacylase | U59433 | <i>Bacillus subtilis</i> | 538 | 45 |
| ORF311 | 346784 | 346437 | beta-ketoacyl-acyl carrier protein synthase III (fabH) | AE000540 | <i>Helicobacter pylori</i> | 273 | 50 |
| ORF312 | 347029 | 346715 | beta-ketoacyl-acyl carrier protein synthase III | M77744 | <i>Escherichia coli</i> | 265 | 63 |
| ORF313 | 347034 | 347723 | recombination protein | D90916 | <i>Synechocystis sp.</i> | 363 | 42 |
| ORF314 | 348075 | 350459 | putative | | | | |
| ORF315 | 350598 | 351071 | putative | | | | |
| ORF316 | 351075 | 352175 | rifampicin resistance protein | L22690 | <i>Rickettsia rickettsii</i> | 495 | 46 |
| ORF317 | 353291 | 352230 | putative | | | | |
| ORF318 | 353442 | 354467 | pyruvate dehydrogenase E1 component, alpha subunit | D90915 | <i>Synechocystis sp.</i> | 571 | 44 |
| ORF319 | 354451 | 354933 | pyruvate dehydrogenase E1 beta subunit | U09137 | <i>Arabidopsis thaliana</i> | 495 | 59 |
| ORF320 | 355000 | 355449 | pyruvate dehydrogenase E1 component, beta subunit | U38804 | <i>Porphyra purpurea</i> | 336 | 47 |
| ORF321 | 355448 | 356743 | F23B12.5 | Z77659 | <i>Caenorhabditis elegans</i> | 759 | 46 |
| ORF322 | 355953 | 355642 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|--------------------------------|-------|----|
| ORF323 | 359310 | 356827 | glycogen phosphorylase B | U47025 | <i>Homo sapiens</i> | 2193 | 57 |
| ORF324 | 359120 | 359377 | putative | | | | |
| ORF325 | 359525 | 359908 | putative | | | | |
| ORF326 | 361290 | 359947 | DnaA | D89066 | <i>Staphylococcus aureus</i> | 375 | 46 |
| ORF327 | 363785 | 361362 | hypothetical | U32781 | <i>Haemophilus influenzae</i> | 394 | 44 |
| ORF328 | 364496 | 363888 | putative | | | | |
| ORF329 | 364832 | 365290 | putative | | | | |
| ORF330 | 365304 | 365669 | dpi | M76470 | <i>Escherichia coli</i> | 160 | 45 |
| ORF331 | 366599 | 365667 | NADPH thioredoxin reductase | AC002329 | <i>Arabidopsis thaliana</i> | 975 | 60 |
| ORF332 | 367291 | 369030 | ribosomal protein S1 (rpS1) | U32801 | <i>Haemophilus influenzae</i> | 1209 | 41 |
| ORF333 | 369134 | 369808 | NusA | U74759 | <i>Chlamydia trachomatis</i> | 995 | 87 |
| ORF334 | 369917 | 370438 | NusA | U74759 | <i>Chlamydia trachomatis</i> | 760 | 87 |
| ORF335 | 370365 | 372647 | | U74759 | <i>Chlamydia trachomatis</i> | 2173 | 61 |
| ORF336 | 372557 | 373066 | initiation factor IF2-beta (infB; gtg start codon) | X00513 | <i>Escherichia coli</i> | 333 | 39 |
| ORF337 | 373020 | 373442 | ORF6 gene product | Z18631 | <i>Bacillus subtilis</i> | 192 | 34 |
| ORF338 | 373467 | 374195 | tRNA pseudouridine 55 synthase | D90917 | <i>Synechocystis sp.</i> | 358 | 47 |
| ORF339 | 374176 | 375099 | hypothetical 34.6 kD protein in rpsT-ileS intergenic region | AE000113 | <i>Escherichia coli</i> | 395 | 39 |
| ORF340 | 375676 | 375083 | hypothetical GTP-binding protein in pth 3' region | AE000219 | <i>Escherichia coli</i> | 507 | 53 |
| ORF341 | 376173 | 375634 | hypothetical | U32723 | <i>Haemophilus influenzae</i> | 480 | 59 |
| ORF342 | 376564 | 377643 | YscU | U08019 | <i>Yersinia enterocolitica</i> | 538 | 37 |
| ORF343 | 377956 | 379773 | lcrD gene product | X67771 | <i>Yersinia enterocolitica</i> | 1302 | 47 |
| ORF344 | 379781 | 380425 | putative | | | | |
| ORF345 | 380281 | 381000 | putative | | | | |
| ORF346 | 381008 | 381460 | putative | | | | |
| ORF347 | 381460 | 383037 | 4-alpha-glucanotransferase | L37874 | <i>Clostridium butyricum</i> | 302 | 38 |
| ORF348 | 383257 | 383523 | ribosomal protein L28 (rpL28) | U32776 | <i>Haemophilus influenzae</i> | 175 | 55 |
| ORF349 | 383553 | 385304 | hypothetical protein | D90901 | <i>Synechocystis sp.</i> | 565 | 38 |
| ORF350 | 385397 | 386458 | comE ORF1 | D64002 | <i>Synechocystis sp.</i> | 187 | 10 |
| ORF351 | 387242 | 386514 | putative | | | | |
| ORF352 | 388764 | 387013 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|-------------------------------------|-------|----|
| ORF353 | 390120 | 390932 | methylentetrahydrofolate dehydrogenase | D64000 | <i>Synechocystis sp.</i> | 588 | 53 |
| ORF354 | 390919 | 391818 | f351; Residues 1-121 are 100 pct identical to YOJL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YOJK_ECOLI SW: P33943 | AE000310 | <i>Escherichia coli</i> | 186 | 39 |
| ORF355 | 392379 | 391885 | small protein | D90914 | <i>Synechocystis sp.</i> | 387 | 46 |
| ORF356 | 392582 | 392986 | putative | | | | |
| ORF357 | 392776 | 393684 | putative | | | | |
| ORF358 | 394151 | 394804 | RecF protein | D90907 | <i>Synechocystis sp.</i> | 232 | 34 |
| ORF359 | 394928 | 395308 | putative | | | | |
| ORF360 | 395259 | 395990 | putative | | | | |
| ORF361 | 397815 | 395953 | hypothetical | U32773 | <i>Haemophilus influenzae</i> | 391 | 36 |
| ORF362 | 398850 | 397831 | H. influenzae predicted coding region HI0807 | U32763 | <i>Haemophilus influenzae</i> | 580 | 39 |
| ORF363 | 400085 | 399099 | putative | | | | |
| ORF364 | 401245 | 400073 | YtgC | AF008220 | <i>Bacillus subtilis</i> | 244 | 30 |
| ORF365 | 401474 | 401136 | putative | | | | |
| ORF366 | 402199 | 401423 | unknown | U52850 | <i>Erysipelothrix rhusiopathiae</i> | 534 | 46 |
| ORF367 | 403193 | 402186 | putative | | | | |
| ORF368 | 403650 | 404165 | putative | | | | |
| ORF369 | 404343 | 405914 | adenine nucleotide translocase | Z49227 | <i>Arabidopsis thaliana</i> | 1280 | 55 |
| ORF370 | 405984 | 407327 | putative | | | | |
| ORF371 | 407712 | 408806 | putative | | | | |
| ORF372 | 410439 | 409075 | putative | | | | |
| ORF373 | 411826 | 410954 | putative | | | | |
| ORF374 | 412482 | 414302 | lepA gene product | X91655 | <i>Bacillus subtilis</i> | 1827 | 59 |
| ORF375 | 415402 | 414407 | 6-phosphogluconate dehydrogenase, decarboxylating (gnd) | U32737 | <i>Haemophilus influenzae</i> | 687 | 51 |
| ORF376 | 415848 | 415237 | 6-phosphogluconate dehydrogenase, 6PGD [Ceratitis capitata=medflies, Peptide, 481 aa] | S67873 | <i>Ceratitis capitata</i> | 695 | 64 |
| ORF377 | 417131 | 415866 | tyrosyl-tRNA synthetase (tyrS) | J01719 | <i>Escherichia coli</i> | 821 | 45 |
| ORF378 | 417258 | 417566 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | % |
|--------|--------|--------|--|----------|--|-------|----|
| ORF379 | 418326 | 417454 | whiG-Stv gene product | X68709 | <i>Streptovorticillium griseocarneum</i> | 464 | 41 |
| ORF380 | 420057 | 418426 | FLHA gene product | X63698 | <i>Bacillus subtilis</i> | 455 | 49 |
| ORF381 | 420448 | 420720 | ferredoxin IV | M59855 | <i>Rhodobacter capsulatus</i> | 174 | 63 |
| ORF382 | 420980 | 421552 | putative | | | | |
| ORF383 | 421556 | 422029 | putative | | | | |
| ORF384 | 422461 | 422925 | putative | | | | |
| ORF385 | 423562 | 424320 | putative | | | | |
| ORF386 | 424250 | 424591 | putative | | | | |
| ORF387 | 424830 | 426047 | putative | | | | |
| ORF388 | 426240 | 427397 | putative | | | | |
| ORF389 | 428841 | 430703 | GepE | D90908 | <i>Synechocystis</i> sp. | 877 | 47 |
| ORF390 | 430694 | 431446 | YfiH | U50134 | <i>Escherichia coli</i> | 136 | 35 |
| ORF391 | 431597 | 432100 | putative | | | | |
| ORF392 | 432165 | 432779 | putative | | | | |
| ORF393 | 433272 | 432832 | dihydrolipoamide succinyltransferase (sucB) | U32839 | <i>Haemophilus influenzae</i> | 475 | 64 |
| ORF394 | 433925 | 433227 | dihydrolipoamide succinyltransferase (sucB) | U32839 | <i>Haemophilus influenzae</i> | 332 | 45 |
| ORF395 | 436678 | 433934 | alpha-ketoglutarate dehydrogenase | U41762 | <i>Rhodobacter capsulatus</i> | 1530 | 44 |
| ORF396 | 437176 | 438357 | oxygen-independent coproporphyrinogen III oxidase (hemN) | AE000628 | <i>Helicobacter pylori</i> | 442 | 42 |
| ORF397 | 440317 | 438518 | putative | | | | |
| ORF398 | 440001 | 440345 | putative | | | | |
| ORF399 | 441233 | 440517 | ORF f286 | U18997 | <i>Escherichia coli</i> | 168 | 45 |
| ORF400 | 440719 | 441012 | putative | | | | |
| ORF401 | 442192 | 441230 | putative | | | | |
| ORF402 | 442888 | 442343 | putative | | | | |
| ORF403 | 442371 | 442961 | putative | | | | |
| ORF404 | 443578 | 443003 | [karp] gene products | M86605 | <i>Chlamydia trachomatis</i> | 505 | 78 |
| ORF405 | 444500 | 443526 | aminopeptidase | D17450 | <i>Mycoplasma salivarium</i> | 273 | 39 |
| ORF406 | 444842 | 444528 | putative | | | | |
| ORF407 | 445009 | 444743 | putative | L39923 | <i>Mycobacterium leprae</i> | 133 | 33 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|-------------------------------|-------|----|
| ORF408 | 445718 | 445182 | putative | | | | |
| ORF409 | 445807 | 447804 | SulP | U18908 | <i>Zea mays</i> | 1307 | 52 |
| ORF410 | 448738 | 447803 | putative | | | | |
| ORF411 | 449628 | 448618 | RuvB protein | U38840 | <i>Thermotoga maritima</i> | 845 | 53 |
| ORF412 | 450298 | 450867 | deoxycytidine triphosphate deaminase (dcd) | AE000554 | <i>Helicobacter pylori</i> | 573 | 58 |
| ORF413 | 450713 | 451207 | putative | | | | |
| ORF414 | 451211 | 452452 | hemolysin | D90914 | <i>Synechocystis sp.</i> | 227 | 39 |
| ORF415 | 452448 | 453659 | similar to [SwissProt Accession Number P37908] | D90888 | <i>Escherichia coli</i> | 96 | 33 |
| ORF416 | 454843 | 453725 | NifS gene product | L34879 | <i>Anabaena azollae</i> | 533 | 38 |
| ORF417 | 455608 | 454865 | hypothetical protein | D90908 | <i>Synechocystis sp.</i> | 371 | 36 |
| ORF418 | 456243 | 457007 | putative | | | | |
| ORF419 | 457016 | 457708 | putative | | | | |
| ORF420 | 458368 | 457979 | unknown | D26185 | <i>Bacillus subtilis</i> | 152 | 36 |
| ORF421 | 459496 | 458372 | mutY homolog | U63329 | <i>Homo sapiens</i> | 466 | 46 |
| ORF422 | 459493 | 460194 | hypothetical protein | D90914 | <i>Synechocystis sp.</i> | 98 | 38 |
| ORF423 | 461446 | 460355 | putative | | | | |
| ORF424 | 462298 | 461450 | putative | | | | |
| ORF425 | 462444 | 463349 | enoyl-ACP reductase | Y13861 | <i>Nicotiana tabacum</i> | 1008 | 69 |
| ORF426 | 464241 | 463342 | putative | | | | |
| ORF427 | 464574 | 465065 | putative | | | | |
| ORF428 | 465129 | 465611 | putative | | | | |
| ORF429 | 465571 | 466317 | putative | | | | |
| ORF430 | 466317 | 467093 | H. pylori predicted coding region HP0152 | AE000536 | <i>Helicobacter pylori</i> | 246 | 36 |
| ORF431 | 466999 | 467502 | putative | | | | |
| ORF432 | 469691 | 467715 | unidentified transporter-ATP binding | Z82044 | <i>Bacillus subtilis</i> | 496 | 45 |
| ORF433 | 470691 | 469660 | acetyl-CoA carboxylase subunit | AF008220 | <i>Bacillus subtilis</i> | 781 | 52 |
| ORF434 | 472010 | 470709 | putative | | | | |
| ORF435 | 471545 | 471799 | putative | | | | |
| ORF436 | 472359 | 472045 | putative | | | | |
| ORF437 | 473523 | 472732 | orf1 | X75413 | <i>Escherichia coli</i> | 313 | 42 |
| ORF438 | 474889 | 473441 | murE gene product | Z15056 | <i>Bacillus subtilis</i> | 679 | 37 |
| ORF439 | 477323 | 475365 | penicillin-binding protein 2 | X59630 | <i>Neisseria meningitidis</i> | 451 | 42 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|-------------------------------|-------|----|
| ORF440 | 478496 | 477597 | hypothetical protein | D90906 | <i>Synechocystis sp.</i> | 534 | 52 |
| ORF441 | 478722 | 479273 | putative | | | | |
| ORF442 | 479277 | 479705 | putative | | | | |
| ORF443 | 480050 | 481450 | chromosomal replication initiator protein | D90909 | <i>Synechocystis sp.</i> | 793 | 40 |
| ORF444 | 481469 | 482053 | DnaA | U35673 | <i>Borrelia burgdorferi</i> | 157 | 37 |
| ORF445 | 482600 | 482025 | OrfH | | | | |
| ORF446 | 482654 | 484204 | putative | Z37111 | <i>Vibrio alginolyticus</i> | 801 | 49 |
| | | | NADH:ubiquinone oxidoreductase subunit B | | | | |
| ORF447 | 484211 | 485170 | NADH:ubiquinone oxidoreductase (GP:Z37111 4) | U32702 | <i>Haemophilus influenzae</i> | 258 | 48 |
| ORF448 | 485170 | 485838 | NADH:ubiquinone oxidoreductase | Z37111 | <i>Vibrio alginolyticus</i> | 543 | 55 |
| ORF449 | 485813 | 486580 | unidentified protein of Na ⁺ -translocating NADH-quinone reductase | D49364 | <i>Vibrio alginolyticus</i> | 488 | 48 |
| ORF450 | 486976 | 486638 | putative | | | | |
| ORF451 | 489071 | 487764 | putative | | | | |
| ORF452 | 489341 | 489090 | putative | | | | |
| ORF453 | 489958 | 489152 | putative | | | | |
| ORF454 | 490549 | 489962 | putative | | | | |
| ORF455 | 491163 | 490522 | putative | | | | |
| ORF456 | 491396 | 491112 | putative | | | | |
| ORF457 | 492121 | 491390 | putative | | | | |
| ORF458 | 492304 | 494838 | ClpC adenosine triphosphatase | U02604 | <i>Bacillus subtilis</i> | 2370 | 46 |
| ORF459 | 495943 | 494822 | hypothetical protein in purB 5' region | AE000213 | <i>Escherichia coli</i> | 927 | 53 |
| ORF460 | 496011 | 496565 | putative | | | | |
| ORF461 | 496569 | 497228 | putative | | | | |
| ORF462 | 497358 | 497834 | putative | | | | |
| ORF463 | 497770 | 498327 | putative | | | | |
| ORF464 | 499209 | 499589 | putative | | | | |
| ORF465 | 499520 | 499792 | putative | | | | |
| ORF466 | 500774 | 504169 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 1215 | 45 |
| ORF467 | 504139 | 504600 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 319 | 47 |
| ORF468 | 504865 | 506877 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 992 | 42 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|--------|---------------------------|-------|----|
| ORF469 | 506790 | 507671 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 739 | 46 |
| ORF470 | 507718 | 510507 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 1813 | 42 |
| ORF471 | 508325 | 507912 | putative | | | | |
| ORF472 | 510660 | 513440 | POMP90A precursor | U65942 | <i>Chlamydia psittaci</i> | 1830 | 46 |
| ORF473 | 514965 | 513787 | hypothetical | D83026 | <i>Bacillus subtilis</i> | 482 | 48 |
| ORF474 | 517347 | 515419 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 1554 | 51 |
| ORF475 | 517058 | 517363 | putative | | | | |
| ORF476 | 517798 | 517277 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 222 | 41 |
| ORF477 | 518200 | 517847 | POMP91B precursor | U65943 | <i>Chlamydia psittaci</i> | 162 | 42 |
| ORF478 | 518300 | 521146 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 1900 | 45 |
| ORF479 | 521392 | 522948 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | 490 | 39 |
| ORF480 | 523244 | 524809 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 507 | 35 |
| ORF481 | 524379 | 524125 | putative | | | | |
| ORF482 | 524649 | 526238 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 969 | 41 |
| ORF483 | 526265 | 527104 | putative | | | | |
| ORF484 | 526947 | 526702 | putative | | | | |
| ORF485 | 526975 | 528450 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 197 | 48 |
| ORF486 | 528408 | 529199 | putative outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 154 | 37 |
| ORF487 | 530612 | 529542 | putative | | | | |
| ORF488 | 531656 | 530616 | putative | | | | |
| ORF489 | 533974 | 532067 | putative | | | | |
| ORF490 | 536432 | 534324 | putative | | | | |
| ORF491 | 537150 | 536707 | putative | | | | |
| ORF492 | 537928 | 537080 | putative | | | | |
| ORF493 | 538438 | 537932 | putative | | | | |
| ORF494 | 538737 | 538333 | putative | | | | |
| ORF495 | 539594 | 539127 | putative | | | | |
| ORF496 | 541215 | 539590 | putative | | | | |
| ORF497 | 542571 | 541282 | putative | | | | |
| ORF498 | 543014 | 542457 | putative | | | | |
| ORF499 | 543369 | 542962 | putative | | | | |
| ORF500 | 543809 | 546628 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 506 | 89 |
| ORF501 | 546619 | 549525 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | 128 | 50 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|---------------------------------|-------|----|
| ORF502 | 547293 | 546994 | putative | | | | |
| ORF503 | 549699 | 550523 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 96 | 32 |
| ORF504 | 550490 | 551551 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 223 | 33 |
| ORF505 | 551448 | 552623 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 139 | 46 |
| ORF506 | 552652 | 555117 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 487 | 48 |
| ORF507 | 555029 | 555493 | putative | | | | |
| ORF508 | 558006 | 555673 | putative | | | | |
| ORF509 | 559694 | 558162 | putative | | | | |
| ORF510 | 558208 | 558573 | putative | | | | |
| ORF511 | 561692 | 559899 | putative | | | | |
| ORF512 | 561412 | 561708 | putative | | | | |
| ORF513 | 563942 | 561777 | 1,4-alpha-glucan branching enzyme | X73903 | <i>Streptomyces coelicolor</i> | 1743 | 45 |
| ORF514 | 564969 | 563950 | putative | | | | |
| ORF515 | 566204 | 564936 | YqeV | D84432 | <i>Bacillus subtilis</i> | 639 | 38 |
| ORF516 | 567717 | 566302 | putative GTPase required for high frequency lysogenization by bacteriophage lambda | U00005 | <i>Escherichia coli</i> | 686 | 41 |
| ORF517 | 568526 | 567708 | putative | | | | |
| ORF518 | 569467 | 568742 | putative | | | | |
| ORF519 | 571065 | 569431 | putative | | | | |
| ORF520 | 571828 | 571118 | arginine-binding periplasmic protein 1 precursor | AE000188 | <i>Escherichia coli</i> | 197 | 45 |
| ORF521 | 572202 | 573308 | putative | | | | |
| ORF522 | 573146 | 575056 | putative | | | | |
| ORF523 | 575023 | 575916 | carboxysome formation protein | D90901 | <i>Synechocystis sp.</i> | 557 | 59 |
| ORF524 | 577891 | 576497 | putative | | | | |
| ORF525 | 578914 | 578204 | putative | | | | |
| ORF526 | 579924 | 578857 | putative | | | | |
| ORF527 | 580187 | 579858 | protein kinase C inhibitor | D90906 | <i>Synechocystis sp.</i> | 260 | 49 |
| ORF528 | 580017 | 580406 | putative | | | | |
| ORF529 | 581086 | 580187 | Yer156cp | U18917 | <i>Saccharomyces cerevisiae</i> | 176 | 34 |
| ORF530 | 581367 | 581828 | putative | | | | |
| ORF531 | 581678 | 582367 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|---------------------------------|-------|-----|
| ORF532 | 582361 | 583428 | putative | | | | |
| ORF533 | 584690 | 583431 | putative | | | | |
| ORF534 | 585237 | 584950 | putative | | | | |
| ORF535 | 585626 | 586888 | hypothetical protein | D64004 | <i>Synechocystis</i> sp. | 805 | 45 |
| ORF536 | 586846 | 587907 | putative | | | | |
| ORF537 | 589049 | 588180 | putative | | | | |
| ORF538 | 590500 | 589301 | putative | | | | |
| ORF539 | 590755 | 592458 | aminoacyl-tRNA synthetase | L25105 | <i>Chlamydia trachomatis</i> | 2125 | 71 |
| ORF540 | 592526 | 592903 | has homology to putative heat shock proteins of <i>Bacillus subtilis</i> and <i>Clostridium acetobutylicum</i> ; ORF-A; putative | L25105 | <i>Chlamydia trachomatis</i> | 324 | 59 |
| ORF541 | 592836 | 593747 | Possible negative regulator of CIRCE element; Homologs in <i>B. subtilis</i> and <i>Clostridia</i> spp. referred to as <i>hrcA</i> or <i>orfA</i> | U52216 | <i>Chlamydia trachomatis</i> | 960 | 65 |
| ORF542 | 593747 | 594298 | grpE | M62819 | <i>Chlamydia trachomatis</i> | 661 | 71 |
| ORF543 | 594331 | 595947 | DnaK protein homolog; 71,550 Da; putative | M69227 | <i>Chlamydia pneumoniae</i> | 2619 | 100 |
| ORF544 | 595905 | 596309 | DnaK protein homolog; 71,550 Da; putative | M69227 | <i>Chlamydia pneumoniae</i> | 674 | 100 |
| ORF545 | 596514 | 597215 | putative | | | | |
| ORF546 | 597184 | 597957 | vacB gene product | U14003 | <i>Escherichia coli</i> | 306 | 48 |
| ORF547 | 597755 | 598612 | ORF-2 | D11024 | <i>Shigella flexneri</i> | 168 | 46 |
| ORF548 | 598602 | 599204 | homologous to DNA glycosylases; hypothetical | D83026 | <i>Bacillus subtilis</i> | 374 | 47 |
| ORF549 | 599373 | 599939 | putative | | | | |
| ORF550 | 600903 | 602072 | hemolysin | X73141 | <i>Serpulina hyodysenteriae</i> | 362 | 36 |
| ORF551 | 602240 | 602587 | hypothetical protein | D90908 | <i>Synechocystis</i> sp. | 182 | 35 |
| ORF552 | 602637 | 603272 | putative | | | | |
| ORF553 | 603142 | 604512 | putative | | | | |
| ORF554 | 604627 | 605853 | conserved hypothetical protein | AE000579 | <i>Helicobacter pylori</i> | 423 | 40 |
| ORF555 | 605790 | 606620 | putative | | | | |
| ORF556 | 606571 | 607281 | putative | L14679 | <i>Lactococcus lactis</i> | 384 | 45 |
| ORF557 | 609004 | 607355 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|---------------------------------|-------|----|
| ORF558 | 610906 | 609932 | putative | | | | |
| ORF559 | 611786 | 611004 | diaminopimelate epimerase | D90917 | <i>Synechocystis</i> sp. | 207 | 55 |
| ORF560 | 612333 | 611746 | ATP-dependent Clp protease proteolytic subunit | D90915 | <i>Synechocystis</i> sp. | 389 | 44 |
| ORF561 | 613897 | 612341 | serine hydroxymethyltransferase | D90903 | <i>Synechocystis</i> sp. | 909 | 52 |
| ORF562 | 615179 | 616279 | putative | | | | |
| ORF563 | 616610 | 617383 | putative | | | | |
| ORF564 | 618796 | 617810 | ORF o328 | U18997 | <i>Escherichia coli</i> | 413 | 45 |
| ORF565 | 620004 | 618826 | branched chain alpha-keto acid dehydrogenase E2 | M97391 | <i>Bacillus subtilis</i> | 688 | 41 |
| ORF566 | 619649 | 619918 | putative | | | | |
| ORF567 | 621265 | 620021 | Hypothetical protein | Y14083 | <i>Bacillus subtilis</i> | 727 | 37 |
| ORF568 | 622359 | 621265 | hypothetical | U32691 | <i>Haemophilus influenzae</i> | 294 | 52 |
| ORF569 | 623420 | 622560 | rRNA methylase | D90913 | <i>Synechocystis</i> sp. | 244 | 38 |
| ORF570 | 624297 | 623335 | hypothetical protein (SP:P39587) | U67605 | <i>Methanococcus jannaschii</i> | 147 | 35 |
| ORF571 | 624773 | 624174 | riboflavin synthase alpha chain | AE000261 | <i>Escherichia coli</i> | 424 | 50 |
| ORF572 | 625029 | 625484 | ORF 168 | D28752 | <i>Synechococcus</i> sp. | 323 | 43 |
| ORF573 | 625488 | 625883 | YteA | AF008220 | <i>Bacillus subtilis</i> | 172 | 35 |
| ORF574 | 625892 | 626395 | signalpeptidase II | X78084 | <i>Staphylococcus carnosus</i> | 204 | 38 |
| ORF575 | 626444 | 627790 | D-alanine permease (dagA) | U32770 | <i>Haemophilus influenzae</i> | 566 | 33 |
| ORF576 | 627912 | 628607 | putative | | | | |
| ORF577 | 628774 | 629697 | putative | | | | |
| ORF578 | 629660 | 631639 | POMP91A | U65942 | <i>Chlamydia psittaci</i> | 579 | 44 |
| ORF579 | 631725 | 633551 | putative | | | | |
| ORF580 | 633520 | 636957 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 266 | 45 |
| ORF581 | 637232 | 638098 | adhesion protein | D90903 | <i>Synechocystis</i> sp. | 267 | 38 |
| ORF582 | 640648 | 639593 | GTP-binding protein | D90901 | <i>Synechocystis</i> sp. | 759 | 45 |
| ORF583 | 640979 | 640728 | 50S ribosomal protein L27 | U38804 | <i>Porphyra purpurea</i> | 265 | 65 |
| ORF584 | 641327 | 641007 | 50S ribosomal subunit protein L21 | U18997 | <i>Escherichia coli</i> | 210 | 41 |
| ORF585 | 641687 | 642283 | hypothetical protein | D90906 | <i>Synechocystis</i> sp. | 76 | 39 |
| ORF586 | 643023 | 642286 | assimilatory sulfite reductase | L26503 | <i>Saccharomyces cerevisiae</i> | 284 | 42 |
| ORF587 | 643330 | 643076 | putative | | | | |
| ORF588 | 643704 | 643351 | ribosomal protein S10 (rpS10) | U32761 | <i>Haemophilus influenzae</i> | 349 | 69 |

| ORF | Begin | End | Homology | ID | Species | Score | % |
|--------|--------|--------|--|----------|---------------------------------------|-------|-----|
| ORF589 | 645628 | 643676 | translation elongation factor EF-G (fusA) | AE000625 | <i>Helicobacter pylori</i> | 1991 | 58 |
| ORF590 | 645783 | 645538 | elongation factor G (AA 1-691) | X16278 | <i>Thermus aquaticus thermophilus</i> | 170 | 80 |
| ORF591 | 646269 | 645793 | ribosomal protein S7 | Z11567 | <i>Chlamydia trachomatis</i> | 730 | 88 |
| ORF592 | 646751 | 646314 | ribosomal protein S12 (AA 1-123) | X52912 | <i>Cryptomonas phi</i> | 485 | 67 |
| ORF593 | 647848 | 647045 | putative | | | | |
| ORF594 | 648393 | 650336 | ORF of prc gene (alt.) | D00674 | <i>Escherichia coli</i> | 554 | 42 |
| ORF595 | 651016 | 650420 | hypothetical sulfur-rich protein | U41759 | <i>Chlamydia psittaci</i> | 301 | 50 |
| ORF596 | 652956 | 651289 | 60kDa CrP | X53511 | <i>Chlamydia pneumoniae</i> | 2951 | 100 |
| ORF597 | 653395 | 653126 | 9kDa CrP | X53511 | <i>Chlamydia pneumoniae</i> | 502 | 99 |
| ORF598 | 655740 | 654193 | glutamyl-tRNA synthetase homolog | U41759 | <i>Chlamydia psittaci</i> | 2259 | 82 |
| ORF599 | 656508 | 655966 | early stage-specific transcription experimentally demonstrated; early upstream open reading frame (EUO) | L13598 | <i>Chlamydia psittaci</i> | 666 | 62 |
| ORF600 | 658140 | 657022 | unknown | U41759 | <i>Chlamydia psittaci</i> | 950 | 44 |
| ORF601 | 660216 | 658525 | RecJ recombination protein | U41759 | <i>Chlamydia psittaci</i> | 807 | 73 |
| ORF602 | 663238 | 660248 | protein-export membrane protein SecD | D64000 | <i>Synechocystis sp.</i> | 413 | 41 |
| ORF603 | 664461 | 663157 | putative | | | | |
| ORF604 | 665735 | 664635 | putative | | | | |
| ORF605 | 666212 | 666994 | hypothetical protein | | | | |
| ORF606 | 666998 | 667921 | o298; This 298 aa orf is 33 pct identical (24 gaps) to 248 residues of an approx. 256 aa protein CDSA ECOLI SW: P06466 | D64006 | <i>Synechocystis sp.</i> | 538 | 58 |
| | | | | AE000238 | <i>Escherichia coli</i> | 253 | 45 |
| ORF607 | 667909 | 668568 | cytidylate kinase | AE000193 | <i>Escherichia coli</i> | 400 | 48 |
| ORF608 | 668502 | 669203 | hypothetical protein | D90915 | <i>Synechocystis sp.</i> | 225 | 33 |
| ORF609 | 669154 | 670893 | arginyl-tRNA-synthetase | D64006 | <i>Synechocystis sp.</i> | 1365 | 49 |
| ORF610 | 672226 | 670853 | UDP-N-acetylglucosamine enolpyruvyl transferase (murZ) | U32788 | <i>Haemophilus influenzae</i> | 642 | 40 |
| ORF611 | 671137 | 671424 | putative | | | | |
| ORF612 | 672453 | 673001 | putative | | | | |
| ORF613 | 673072 | 674721 | putative | | | | |
| ORF614 | 674549 | 674262 | putative | | | | |
| ORF615 | 675518 | 674796 | ORF246 gene product | X59551 | <i>Escherichia coli</i> | 520 | 43 |
| ORF616 | 676083 | 675499 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|---------------------------------|-------|----|
| ORF617 | 676630 | 676067 | putative | | | | |
| ORF618 | 677016 | 676600 | ORF3 | D10279 | <i>Bacillus subtilis</i> | 361 | 63 |
| ORF619 | 677647 | 677015 | peptide release factor 2 | X99401 | <i>Bacillus firmus</i> | 427 | 43 |
| ORF620 | 677990 | 678259 | unknown | Z49939 | <i>Saccharomyces cerevisiae</i> | 175 | 48 |
| ORF621 | 679444 | 680097 | unknown | D26185 | <i>Bacillus subtilis</i> | 263 | 38 |
| ORF622 | 680097 | 680897 | unknown | D64126 | <i>Bacillus subtilis</i> | 506 | 45 |
| ORF623 | 681637 | 680849 | putative | | | | |
| ORF624 | 681409 | 682281 | putative | | | | |
| ORF625 | 682453 | 682821 | putative | | | | |
| ORF626 | 682763 | 683902 | sensor protein | L39904 | <i>Myxococcus xanthus</i> | 190 | 48 |
| ORF627 | 684616 | 683969 | putative | | | | |
| ORF628 | 685169 | 684534 | putative | | | | |
| ORF629 | 685986 | 685117 | putative | | | | |
| ORF630 | 686278 | 687288 | NtrC/NifA-like protein regulator | U17902 | <i>Escherichia coli</i> | 820 | 45 |
| ORF631 | 687483 | 688151 | putative | | | | |
| ORF632 | 688740 | 689501 | putative | | | | |
| ORF633 | 690242 | 689622 | putative | | | | |
| ORF634 | 690470 | 691126 | unknown | Z48008 | <i>Saccharomyces cerevisiae</i> | 380 | 46 |
| ORF635 | 692600 | 691497 | putative | | | | |
| ORF636 | 692674 | 695064 | phenylalanyl-tRNA synthetase beta-subunit (pheT) | U32810 | <i>Haemophilus influenzae</i> | 593 | 45 |
| ORF637 | 695049 | 696032 | putative | | | | |
| ORF638 | 697964 | 696585 | OppC-like protein | D85103 | <i>Synechococcus sp.</i> | 371 | 37 |
| ORF639 | 699803 | 698274 | OppB gene product | X56347 | <i>Bacillus subtilis</i> | 197 | 40 |
| ORF640 | 701926 | 699788 | AppA | U20909 | <i>Bacillus subtilis</i> | 324 | 43 |
| ORF641 | 703196 | 702567 | putative | | | | |
| ORF642 | 704221 | 703208 | putative | | | | |
| ORF643 | 704240 | 705289 | ferrochelatase | X73417 | <i>Arabidopsis thaliana</i> | 266 | 42 |
| ORF644 | 706070 | 705300 | histidine periplasmic binding protein P29 | U58045 | <i>Campylobacter jejuni</i> | 128 | 31 |
| ORF645 | 706841 | 706254 | conserved hypothetical protein | AE000592 | <i>Helicobacter pylori</i> | 155 | 37 |
| ORF646 | 707596 | 706811 | putative | | | | |
| ORF647 | 708666 | 707677 | ADP-glucose pyrophosphorylase | X55650 | <i>Solanum tuberosum</i> | 595 | 43 |
| ORF648 | 709793 | 709119 | pyrE-F gene product | X71842 | <i>Arabidopsis thaliana</i> | 400 | 44 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|--------|---------------------------------|-------|----|
| ORF649 | 711523 | 710132 | transcription termination factor | J01673 | <i>Escherichia coli</i> | 1251 | 60 |
| ORF650 | 712236 | 711523 | putative | | | | |
| ORF651 | 714734 | 712125 | DNA polymerase I | J04479 | <i>Streptococcus pneumoniae</i> | 1334 | 43 |
| ORF652 | 715759 | 714761 | protease IV | U67512 | <i>Methanococcus jannaschii</i> | 101 | 55 |
| ORF653 | 717538 | 715886 | adenine nucleotide translocase | Z49227 | <i>Arabidopsis thaliana</i> | 832 | 39 |
| ORF654 | 719113 | 720243 | replicative DNA helicase | D26185 | <i>Bacillus subtilis</i> | 776 | 44 |
| ORF655 | 720590 | 722422 | homologous to E.coli gidA | X62540 | <i>Pseudomonas putida</i> | 1575 | 52 |
| ORF656 | 722406 | 723056 | putative | | | | |
| ORF657 | 723551 | 723120 | nucleoside 5'-diphosphate phosphotransferase (EC 2.7.4.6) | J05207 | <i>Myxococcus xanthus</i> | 451 | 62 |
| ORF658 | 724246 | 723626 | Holliday junction DNA helicase (ruvA) | U32716 | <i>Haemophilus influenzae</i> | 293 | 43 |
| ORF659 | 724754 | 724251 | crossover junction endodeoxyribonuclease (ruvC) | U32717 | <i>Haemophilus influenzae</i> | 296 | 53 |
| ORF660 | 725868 | 724900 | putative | | | | |
| ORF661 | 727115 | 726270 | putative | | | | |
| ORF662 | 728126 | 727119 | glyceraldehyde-3-phosphate dehydrogenase | U83198 | <i>Chlamydia trachomatis</i> | 1340 | 75 |
| ORF663 | 728594 | 728208 | ribosomal protein L17 | L33834 | <i>Chlamydia trachomatis</i> | 439 | 82 |
| ORF664 | 729614 | 728604 | RNA polymerase alpha-subunit | L33834 | <i>Chlamydia trachomatis</i> | 1356 | 89 |
| ORF665 | 729778 | 729533 | RNA polymerase alpha-subunit | L33834 | <i>Chlamydia trachomatis</i> | 273 | 82 |
| ORF666 | 730149 | 729751 | ribosomal protein S11 | L33834 | <i>Chlamydia trachomatis</i> | 562 | 90 |
| ORF667 | 730539 | 730174 | ribosomal protein S13 | L33834 | <i>Chlamydia trachomatis</i> | 544 | 89 |
| ORF668 | 731983 | 730598 | homolog | L25077 | <i>Chlamydia trachomatis</i> | 1956 | 83 |
| ORF669 | 732427 | 731996 | ribosomal protein CtrL15e | M80325 | <i>Chlamydia trachomatis</i> | 563 | 77 |
| ORF670 | 732917 | 732423 | ribosomal protein CtrS5e | M80325 | <i>Chlamydia trachomatis</i> | 702 | 84 |
| ORF671 | 733598 | 733320 | ribosomal protein L6 | M60652 | <i>Chlamydia trachomatis</i> | 316 | 87 |
| ORF672 | 733869 | 733492 | ribosomal protein L6 | M60652 | <i>Chlamydia trachomatis</i> | 469 | 77 |
| ORF673 | 734298 | 733900 | ribosomal protein CtrS8e | M80325 | <i>Chlamydia trachomatis</i> | 572 | 82 |
| ORF674 | 734858 | 734319 | ribosomal protein CtrL5e | M80325 | <i>Chlamydia trachomatis</i> | 730 | 90 |
| ORF675 | 735195 | 734863 | ribosomal protein CtrL24e | M80325 | <i>Chlamydia trachomatis</i> | 420 | 70 |
| ORF676 | 735578 | 735342 | ribosomal protein CtrL14e | M80325 | <i>Chlamydia trachomatis</i> | 270 | 95 |
| ORF677 | 735861 | 735604 | ribosomal protein S17e | M80325 | <i>Chlamydia trachomatis</i> | 322 | 77 |
| ORF678 | 736492 | 736079 | 50S ribosomal protein L16 | D90905 | <i>Synechocystis sp.</i> | 439 | 60 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|---|-------|----|
| ORF679 | 737192 | 736524 | ribosomal protein S3 | D64071 | <i>Actinobacillus actinomycetemcomitans</i> | 612 | 58 |
| ORF680 | 737555 | 737211 | ribosomal protein L22 | Z21677 | <i>Thermotoga maritima</i> | 228 | 48 |
| ORF681 | 738688 | 737837 | 50S ribosomal subunit protein L2 | U18997 | <i>Escherichia coli</i> | 769 | 62 |
| ORF682 | 739048 | 738713 | putative | | | | |
| ORF683 | 739736 | 739065 | ribosomal protein L4 | X67014 | <i>Bacillus stearothermophilus</i> | 308 | 46 |
| ORF684 | 740477 | 739773 | ribosomal protein L3 | Z46265 | <i>Thermus aquaticus thermophilus</i> | 463 | 50 |
| ORF685 | 740659 | 740958 | putative | | | | |
| ORF686 | 741722 | 740721 | putative | | | | |
| ORF687 | 742789 | 741827 | methionyl-tRNA formyltransferase | D64001 | <i>Synechocystis sp.</i> | 511 | 48 |
| ORF688 | 743618 | 742782 | UDP-N-acetylglucosamine acyltransferase | L22690 | <i>Rickettsia rickettsii</i> | 542 | 43 |
| ORF689 | 744092 | 743634 | (3R)-hydroxymyristol acyl carrier protein dehydrase | D90910 | <i>Synechocystis sp.</i> | 339 | 55 |
| ORF690 | 744604 | 744107 | UDP-3-O-acyl N-acetylglucosamine deacetylase | D90902 | <i>Synechocystis sp.</i> | 287 | 45 |
| ORF691 | 744953 | 744498 | UDP-3-O-acyl-GlcNAc deacetylase | U67855 | <i>Pseudomonas aeruginosa</i> | 262 | 51 |
| ORF692 | 746608 | 744986 | apolipoprotein N-acyltransferase (cute) | U32716 | <i>Haemophilus influenzae</i> | 194 | 50 |
| ORF693 | 747085 | 746621 | low homology to P14 protein of <i>Haemophilus influenzae</i> and 14.2 kDa protein of <i>Escherichia coli</i> | D78189 | <i>Bacillus subtilis</i> | 235 | 37 |
| ORF694 | 747974 | 747219 | polymerase III | M22996 | <i>Bacillus subtilis</i> | 180 | 34 |
| ORF695 | 748594 | 748169 | hypothetical protein | D90914 | <i>Synechocystis sp.</i> | 160 | 43 |
| ORF696 | 749145 | 748573 | putative | | | | |
| ORF697 | 749652 | 749957 | trxA | L39892 | <i>Chlamydia psittaci</i> | 393 | 72 |
| ORF698 | 750446 | 749979 | spoU | L39892 | <i>Chlamydia psittaci</i> | 559 | 72 |
| ORF699 | 751219 | 750446 | mip | L39892 | <i>Chlamydia psittaci</i> | 948 | 60 |
| ORF700 | 753042 | 751291 | aspartyl-tRNA synthetase | D90910 | <i>Synechocystis sp.</i> | 1347 | 47 |
| ORF701 | 754309 | 753020 | histidine-tRNA ligase | Z17214 | <i>Streptococcus equisimilis</i> | 757 | 44 |
| ORF702 | 755120 | 756175 | hexosephosphate transport protein | M89480 | <i>Salmonella typhimurium</i> | 870 | 49 |
| ORF703 | 756120 | 756485 | hexosephosphate transport protein | M89479 | <i>Escherichia coli</i> | 321 | 45 |
| ORF704 | 756499 | 760227 | DNA polymerase III alpha-subunit (dnaE) | AE000646 | <i>Helicobacter pylori</i> | 1977 | 42 |
| ORF705 | 761217 | 760297 | putative | | | | |
| ORF706 | 761297 | 761809 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|--------------------------------------|-------|----|
| ORF707 | 761782 | 762282 | putative | | | | |
| ORF708 | 762260 | 762895 | putative | | | | |
| ORF709 | 762867 | 763316 | hypothetical protein | D90908 | <i>Synechocystis</i> sp. | 177 | 43 |
| ORF710 | 763780 | 763325 | putative | | | | |
| ORF711 | 763861 | 765168 | DD-carboxypeptidase | M85047 | <i>Bacillus subtilis</i> | 292 | 37 |
| ORF712 | 766809 | 765697 | fmu and fmv protein | D90902 | <i>Synechocystis</i> sp. | 130 | 36 |
| ORF713 | 768051 | 766888 | putative | | | | |
| ORF714 | 768566 | 768321 | putative | | | | |
| ORF715 | 769342 | 768551 | putative | | | | |
| ORF716 | 770532 | 769378 | putative | | | | |
| ORF717 | 771451 | 770804 | putative | | | | |
| ORF718 | 773058 | 771847 | 3-phosphoglycerate kinase | U83197 | <i>Chlamydia trachomatis</i> | 1540 | 72 |
| ORF719 | 773094 | 773456 | putative | | | | |
| ORF720 | 774376 | 773093 | putative phosphate permease | U84890 | <i>Mesembryanthemum crystallinum</i> | 870 | 45 |
| ORF721 | 775123 | 774380 | putative | | | | |
| ORF722 | 775398 | 774916 | putative | | | | |
| ORF723 | 775046 | 776077 | sporulation protein | M57689 | <i>Bacillus subtilis</i> | 698 | 43 |
| ORF724 | 776070 | 777041 | was dppE | U00039 | <i>Escherichia coli</i> | 565 | 56 |
| ORF725 | 777964 | 777536 | orf288; translated orf similarity to SWISS-PROT: YGI2_PSEPU hypothetical 32.4 kDa protein of <i>Pseudomonas putida</i> | Y10436 | <i>Coxiella burnetii</i> | 256 | 46 |
| ORF726 | 778176 | 777904 | B.subtilis genes rpmH, mpA, 50kd, gidA and gidB | X62539 | <i>Bacillus subtilis</i> | 112 | 37 |
| ORF727 | 778621 | 779334 | putative | | | | |
| ORF728 | 781173 | 780307 | f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089 | AE000263 | <i>Escherichia coli</i> | 603 | 40 |
| ORF729 | 781526 | 781116 | f406; This 406 aa orf is 28 pct identical (12 gaps) to 264 residues of an approx. 440 aa protein YAOA SCHPO SW: O10089 | AE000263 | <i>Escherichia coli</i> | 258 | 45 |
| ORF730 | 782784 | 781555 | f423; This 423 aa orf is 29 pct identical (1 gaps) to 172 residues of an approx. 488 aa protein YC24 CYAPA SW: P48260 | AE000263 | <i>Escherichia coli</i> | 197 | 44 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|--------|-----------------------------------|-------|----|
| ORF731 | 783572 | 782805 | hypothetical chloroplast ORF 16 | U38804 | <i>Porphyra purpurea</i> | 597 | 52 |
| ORF732 | 785032 | 783581 | ABC transporter subunit | D64004 | <i>Synechocystis sp.</i> | 1720 | 62 |
| ORF733 | 786412 | 785360 | putative | | | | |
| ORF734 | 788429 | 786450 | bbp | Y14206 | <i>Streptomyces coelicolor</i> | 148 | 55 |
| ORF735 | 788944 | 788528 | penicillin-binding protein 3 | X84053 | <i>Pseudomonas aeruginosa</i> | 148 | 38 |
| ORF736 | 789758 | 788901 | putative | | | | |
| ORF737 | 790332 | 791504 | major outer membrane protein | M64064 | <i>Chlamydia pneumoniae</i> | 2028 | 99 |
| ORF738 | 791846 | 792721 | ribosomal protein S2 | U60196 | <i>Chlamydia trachomatis</i> | 904 | 70 |
| ORF739 | 792724 | 793569 | elongation factor Ts | U60196 | <i>Chlamydia trachomatis</i> | 1023 | 71 |
| ORF740 | 793580 | 794323 | UMP kinase | U60196 | <i>Chlamydia trachomatis</i> | 891 | 72 |
| ORF741 | 794304 | 794843 | ribosome-releasing factor | U60196 | <i>Chlamydia trachomatis</i> | 673 | 73 |
| ORF742 | 795217 | 795732 | unknown | D26185 | <i>Bacillus subtilis</i> | 105 | 42 |
| ORF743 | 795722 | 796795 | unknown | D26185 | <i>Bacillus subtilis</i> | 208 | 33 |
| ORF744 | 798735 | 797053 | putative | L33796 | <i>Vibrio cholerae</i> | 386 | 34 |
| ORF745 | 798823 | 798681 | putative | | | | |
| ORF746 | 799297 | 799578 | putative | | | | |
| ORF747 | 801313 | 799808 | Pkn5 | U40656 | <i>Myxococcus xanthus</i> | 345 | 33 |
| ORF748 | 802453 | 801332 | putative | | | | |
| ORF749 | 803299 | 802457 | putative | | | | |
| ORF750 | 803811 | 803290 | putative | | | | |
| ORF751 | 805151 | 803826 | YscN | U02499 | <i>Yersinia enterocolitica</i> | 1185 | 53 |
| ORF752 | 805860 | 805156 | putative | | | | |
| ORF753 | 806604 | 806332 | putative | | | | |
| ORF754 | 806913 | 806608 | putative | | | | |
| ORF755 | 808222 | 806903 | putative | | | | |
| ORF756 | 808751 | 808146 | putative | | | | |
| ORF757 | 809437 | 808673 | putative | | | | |
| ORF758 | 809939 | 809454 | putative | | | | |
| ORF759 | 811235 | 810213 | delta-aminolevulinic synthase (EC 2.3.1.37) | M30785 | <i>Escherichia coli</i> | 172 | 40 |
| ORF760 | 811779 | 813056 | DNA gyrase subunit B | U35453 | <i>Clostridium acetobutylicum</i> | 584 | 38 |
| ORF761 | 812890 | 812516 | putative | | | | |
| ORF762 | 812954 | 813583 | DNA gyrase subunit B | Z19108 | <i>Spiroplasma citri</i> | 371 | 39 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|-----------------------------------|-------|-----|
| ORF763 | 813587 | 815023 | gytA | X92503 | <i>Mycobacterium smegmatis</i> | 414 | 55 |
| ORF764 | 815420 | 815746 | putative | | | | |
| ORF765 | 816036 | 817010 | orf-X; hypothetical protein; Method: conceptual translation supplied by author | U48870 | <i>Bacillus subtilis</i> | 569 | 47 |
| ORF766 | 817111 | 817356 | unknown | Z74024 | <i>Mycobacterium tuberculosis</i> | 114 | 34 |
| ORF767 | 817791 | 818609 | 3-deoxy-d-manno-octulosonic acid 8- phosphate synthetase | Z50747 | <i>Chlamydia psittaci</i> | 1112 | 78 |
| ORF768 | 818609 | 819094 | protein of unknown function | Z50747 | <i>Chlamydia psittaci</i> | 545 | 65 |
| ORF769 | 819104 | 819823 | ATP binding protein | U72493 | <i>Chlamydia trachomatis</i> | 1099 | 88 |
| ORF770 | 820722 | 819826 | putative | | | | |
| ORF771 | 822313 | 821000 | putative | | | | |
| ORF772 | 823503 | 822238 | putative | | | | |
| ORF773 | 823678 | 825612 | putative | | | | |
| ORF774 | 825461 | 826312 | putative | | | | |
| ORF775 | 827280 | 826645 | putative | | | | |
| ORF776 | 828604 | 827171 | 76 kDa protein | L23921 | <i>Chlamydia pneumoniae</i> | 2179 | 100 |
| ORF777 | 830026 | 828713 | 76 kDa protein | L23921 | <i>Chlamydia pneumoniae</i> | 1162 | 100 |
| ORF778 | 831047 | 830085 | mvbB homolog | U50732 | <i>Chlamydia trachomatis</i> | 982 | 58 |
| ORF779 | 831725 | 831051 | mvbB homolog | U50732 | <i>Chlamydia trachomatis</i> | 740 | 65 |
| ORF780 | 832220 | 833098 | T05H10.2 | Z47812 | <i>Caenorhabditis elegans</i> | 407 | 34 |
| ORF781 | 833851 | 833396 | ribosomal protein S4 (rps4) | AF000633 | <i>Helicobacter pylori</i> | 372 | 53 |
| ORF782 | 834068 | 835039 | This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from <i>E. coli</i> . Accession Number X61000 | L22217 | <i>Mycoplasma-like organism</i> | 377 | 49 |
| ORF783 | 835792 | 835127 | uridine kinase | L31783 | <i>Mus musculus</i> | 436 | 43 |
| ORF784 | 837624 | 836116 | ORF f397 | U29581 | <i>Escherichia coli</i> | 92 | 38 |
| ORF785 | 838951 | 840882 | putative | | | | |
| ORF786 | 840869 | 842185 | exodeoxyribonuclease V (recB) | U32811 | <i>Haemophilus influenzae</i> | 409 | 40 |
| ORF787 | 841989 | 843455 | DNA helicase II | U39703 | <i>Mycoplasma genitalium</i> | 110 | 46 |
| ORF788 | 843242 | 844021 | exodeoxyribonuclease V (recB) | U32811 | <i>Haemophilus influenzae</i> | 196 | 40 |
| ORF789 | 845018 | 843987 | MreC protein | M31792 | <i>Escherichia coli</i> | 76 | 53 |
| ORF790 | 846174 | 844990 | aspartate aminotransferase (aspC) | X03629 | <i>Escherichia coli</i> | 754 | 40 |
| ORF791 | 848509 | 846311 | GreA | U02878 | <i>Rickettsia prowazekii</i> | 190 | 35 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|--|----------|---------------------------------|-------|----|
| ORF792 | 848568 | 849014 | putative | | | | |
| ORF793 | 849082 | 850488 | NADH:ubiquinone oxidoreductase subunit A (GP:Z37111_2) | U32702 | <i>Haemophilus influenzae</i> | 445 | 37 |
| ORF794 | 851512 | 850574 | porphobilinogen synthase | U38348 | <i>Chlorobium vibrioforme</i> | 769 | 45 |
| ORF795 | 852064 | 852447 | putative | | | | |
| ORF796 | 852398 | 853690 | putative | | | | |
| ORF797 | 855118 | 854243 | geranylgeranyl pyrophosphate synthase | D85029 | <i>Arabidopsis thaliana</i> | 408 | 41 |
| ORF798 | 855751 | 855128 | f147; This 147 aa orf is 26 pct identical (1 gaps) to 99 residues of an approx. 728 aa protein E2BE_RABIT SW: P47823 | AE000143 | <i>Escherichia coli</i> | 187 | 36 |
| ORF799 | 856551 | 855829 | membrane associated regulatory protein | M28368 | <i>Salmonella typhimurium</i> | 172 | 36 |
| ORF800 | 856730 | 858556 | unknown function | Z32530 | <i>Chlamydia trachomatis</i> | 842 | 35 |
| ORF801 | 858717 | 859601 | exodeoxyribonuclease V (recD) | U32811 | <i>Haemophilus influenzae</i> | 182 | 51 |
| ORF802 | 859591 | 860205 | exonuclease V alpha subunit (AA 1-608) | X04582 | <i>Escherichia coli</i> | 235 | 45 |
| ORF803 | 861132 | 860284 | putative | | | | |
| ORF804 | 861426 | 861163 | 30S ribosomal protein S20 | Z67753 | <i>Odonella sinensis</i> | 153 | 41 |
| ORF805 | 861701 | 862921 | putative | | | | |
| ORF806 | 863026 | 864798 | major sigma factor | U04442 | <i>Chlamydia psittaci</i> | 2661 | 94 |
| ORF807 | 864831 | 865256 | putative | | | | |
| ORF808 | 865226 | 866581 | dihydropterin pyrophosphokinase /dihydropteroate synthase | Y08611 | <i>Pisum sativum</i> | 455 | 48 |
| ORF809 | 866562 | 867119 | dehydrofolate reductase, type I (folA) | U32772 | <i>Haemophilus influenzae</i> | 213 | 49 |
| ORF810 | 867025 | 867816 | M. jannaschii predicted coding region | U67522 | <i>Methanococcus jannaschii</i> | 207 | 36 |
| ORF811 | 867820 | 868497 | MJ0768 | | | | |
| ORF812 | 869743 | 868661 | putative | | | | |
| ORF813 | 870633 | 870094 | RecA | U16739 | <i>Chlamydia trachomatis</i> | 1512 | 87 |
| ORF814 | 871929 | 870646 | unknown function | Z32530 | <i>Chlamydia trachomatis</i> | 308 | 45 |
| ORF815 | 872538 | 872086 | unknown function | Z32530 | <i>Chlamydia trachomatis</i> | 1410 | 63 |
| ORF816 | 873908 | 872517 | putative | | | | |
| ORF817 | 874281 | 874670 | putative | | | | |
| ORF818 | 874582 | 875286 | niR3-like gene product | Z37984 | <i>Azospirillum brasilense</i> | 181 | 32 |
| ORF819 | 877857 | 875377 | ORF1 gene product | X62399 | <i>Escherichia coli</i> | 307 | 42 |
| | | | DNA topoisomerase I | L27797 | <i>Bacillus subtilis</i> | 1488 | 50 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|--------|-------------------------------|-------|----|
| ORF820 | 878446 | 879255 | putative | | | | |
| ORF821 | 880635 | 879268 | sigma factor (ntrA) (AA 1-502) | X05888 | <i>Azotobacter vinelandii</i> | 257 | 47 |
| ORF822 | 882524 | 880593 | DNA helicase II | D90906 | <i>Synechocystis</i> sp. | 1140 | 50 |
| ORF823 | 882612 | 883319 | ipa-57d gene product | X73124 | <i>Bacillus subtilis</i> | 601 | 51 |
| ORF824 | 884155 | 883538 | hypothetical protein | D90915 | <i>Synechocystis</i> sp. | 344 | 39 |
| ORF825 | 884340 | 885611 | 19/20 residue stretch (32-51) identical to N-terminal putative signal sequence of unknown, partly cloned <i>B. subtilis</i> gene.; putative | L19954 | <i>Bacillus subtilis</i> | 456 | 37 |
| ORF826 | 885722 | 887302 | heat shock protein | L12004 | <i>Chlamydia trachomatis</i> | 915 | 39 |
| ORF827 | 887587 | 888153 | bas1 protein | Z34917 | <i>Hordeum vulgare</i> | 474 | 50 |
| ORF828 | 888627 | 888220 | putative | | | | |
| ORF829 | 889330 | 888716 | hypothetical protein | Y14079 | <i>Bacillus subtilis</i> | 223 | 55 |
| ORF830 | 889898 | 889323 | peptidoglycan-associated lipoprotein | X65796 | <i>Escherichia coli</i> | 222 | 50 |
| ORF831 | 891190 | 889898 | TolB | U32470 | <i>Haemophilus influenzae</i> | 280 | 35 |
| ORF832 | 891828 | 891247 | putative | | | | |
| ORF833 | 892421 | 892017 | exbD peptide | M28819 | <i>Escherichia coli</i> | 77 | 48 |
| ORF834 | 893116 | 892421 | inner membrane protein (tolQ) | U32722 | <i>Haemophilus influenzae</i> | 157 | 54 |
| ORF835 | 892521 | 892925 | putative | | | | |
| ORF836 | 893392 | 895419 | inner membrane copper tolerance protein | Z36905 | <i>Escherichia coli</i> | 120 | 35 |
| ORF837 | 895745 | 896527 | unknown | D26185 | <i>Bacillus subtilis</i> | 381 | 41 |
| ORF838 | 896668 | 897558 | succinate dehydrogenase subunit C | Y08563 | <i>Paenibacillus macerans</i> | 253 | 40 |
| ORF839 | 897565 | 899442 | succinate dehydrogenase subunit A | Y08563 | <i>Paenibacillus macerans</i> | 1667 | 57 |
| ORF840 | 899420 | 900229 | succinate dehydrogenase subunit B | Y08563 | <i>Paenibacillus macerans</i> | 656 | 54 |
| ORF841 | 903230 | 900237 | putative | | | | |
| ORF842 | 905081 | 903234 | putative | | | | |
| ORF843 | 906931 | 905045 | sigma factor SibG regulation protein RsbU | D90905 | <i>Synechocystis</i> sp. | 117 | 35 |
| ORF844 | 907248 | 907832 | putative | | | | |
| ORF845 | 907784 | 908128 | putative | | | | |
| ORF846 | 908132 | 908677 | putative | | | | |
| ORF847 | 908589 | 909320 | putative | | | | |
| ORF848 | 909405 | 911465 | putative | | | | |
| ORF849 | 911677 | 912360 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|-------------------------------------|--------|-------------------------------|-------|----|
| ORF850 | 912303 | 912821 | putative | | | | |
| ORF851 | 912937 | 913983 | putative | | | | |
| ORF852 | 915128 | 914067 | putative | | | | |
| ORF853 | 916658 | 915303 | enolase | L29475 | <i>Bacillus subtilis</i> | 1036 | 60 |
| ORF854 | 915627 | 915376 | enolase | U43738 | <i>Mycoplasma pneumoniae</i> | 226 | 65 |
| ORF855 | 917707 | 916853 | excinuclease ABC subunit B (uvrB) | U32804 | <i>Haemophilus influenzae</i> | 724 | 46 |
| ORF856 | 918837 | 917722 | excinuclease ABC subunit B (uvrB) | U32804 | <i>Haemophilus influenzae</i> | 1029 | 54 |
| ORF857 | 919868 | 918837 | tryptophanyl-tRNA synthetase (trpS) | U32746 | <i>Haemophilus influenzae</i> | 376 | 40 |
| ORF858 | 920434 | 919880 | putative | | | | |
| ORF859 | 921187 | 920438 | ORF8 | X82078 | <i>Chlamydia sp.</i> | 164 | 50 |
| ORF860 | 921959 | 921195 | hypothetical protein | X62475 | <i>Chlamydia psittaci</i> | 511 | 44 |
| ORF861 | 923773 | 921995 | Threonyl tRNA Synthetase | Z80360 | <i>Bacillus subtilis</i> | 1476 | 44 |
| ORF862 | 922146 | 922415 | putative | | | | |
| ORF863 | 923943 | 923674 | putative | | | | |
| ORF864 | 924077 | 925006 | putative | | | | |
| ORF865 | 925436 | 925083 | putative | | | | |
| ORF866 | 926524 | 925349 | putative | | | | |
| ORF867 | 927920 | 926433 | putative | | | | |
| ORF868 | 928319 | 927951 | putative | | | | |
| ORF869 | 928963 | 928334 | putative | | | | |
| ORF870 | 929248 | 930987 | DNA mismatch repair protein (mutL) | U32692 | <i>Haemophilus influenzae</i> | 585 | 40 |
| ORF871 | 930995 | 932059 | YqhT | D84432 | <i>Bacillus subtilis</i> | 445 | 39 |
| ORF872 | 932121 | 933515 | putative | | | | |
| ORF873 | 932881 | 932513 | putative | | | | |
| ORF874 | 933485 | 935746 | pulD (tgg start codon) | M32613 | <i>Klebsiella pneumoniae</i> | 210 | 33 |
| ORF875 | 935724 | 937082 | epsE | M96172 | <i>Vibrio cholerae</i> | 890 | 55 |
| ORF876 | 937229 | 938410 | PilG | U32588 | <i>Neisseria gonorrhoeae</i> | 280 | 38 |
| ORF877 | 938281 | 938805 | putative | | | | |
| ORF878 | 938809 | 939255 | putative | | | | |
| ORF879 | 939165 | 939782 | putative | | | | |
| ORF880 | 939760 | 940791 | putative | | | | |
| ORF881 | 940822 | 941106 | putative | | | | |
| ORF882 | 940977 | 941351 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|--------|--------|---|----------|------------------------------------|-------|----|
| ORF883 | 942537 | 941623 | yscT | L25667 | <i>Yersinia pseudotuberculosis</i> | 169 | 44 |
| ORF884 | 942784 | 942500 | yscS | L25667 | <i>Yersinia pseudotuberculosis</i> | 173 | 42 |
| ORF885 | 943149 | 942799 | HcrR | AE000107 | <i>Rhizobium sp. NGR234</i> | 265 | 52 |
| ORF886 | 943029 | 943029 | pathogenicity protein | M64094 | <i>Xanthomonas campestris</i> | 252 | 41 |
| ORF887 | 944055 | 943732 | putative | M74011 | <i>Yersinia enterocolitica</i> | 112 | 33 |
| ORF888 | 944413 | 943994 | putative | | | | |
| ORF889 | 945395 | 944556 | putative | | | | |
| ORF890 | 945853 | 945389 | putative | | | | |
| ORF891 | 946392 | 945751 | HrcJ | U56662 | <i>Erwinia amylovora</i> | 229 | 44 |
| ORF892 | 947410 | 948081 | putative | | | | |
| ORF893 | 949871 | 948915 | ORF YOR196c | Z75104 | <i>Saccharomyces cerevisiae</i> | 702 | 44 |
| ORF894 | 951058 | 949868 | dihydrolipoamide dehydrogenase E3 subunit | M57435 | <i>Bacillus subtilis</i> | 745 | 39 |
| ORF895 | 951249 | 950959 | dihydrolipoamide acetyltransferase E3 subunit | M73535 | <i>Staphylococcus aureus</i> | 166 | 49 |
| ORF896 | 951664 | 952134 | putative | | | | |
| ORF897 | 952674 | 952165 | SNF | X98455 | <i>Bacillus cereus</i> | 229 | 47 |
| ORF898 | 953491 | 952589 | helicase | U39680 | <i>Mycoplasma genitalium</i> | 307 | 42 |
| ORF899 | 953224 | 953495 | F01G4.1 | Z68341 | <i>Caenorhabditis elegans</i> | 133 | 57 |
| ORF900 | 955823 | 955281 | putative | | | | |
| ORF901 | 957082 | 955847 | branched-chain amino acid carrier | Z48676 | <i>Lactobacillus delbrueckii</i> | 297 | 40 |
| ORF902 | 957902 | 957270 | endonuclease III | U11289 | <i>Bacillus subtilis</i> | 317 | 37 |
| ORF903 | 959231 | 957906 | homologous to E.coli 50K | X62539 | <i>Bacillus subtilis</i> | 805 | 45 |
| ORF904 | 959376 | 960284 | phosphatidylserine decarboxylase | U72715 | <i>Chlamydia trachomatis</i> | 776 | 51 |
| ORF905 | 960266 | 961669 | putative | | | | |
| ORF906 | 961856 | 964765 | secretory component | U06928 | <i>Caulobacter crescentus</i> | 1812 | 55 |
| ORF907 | 966855 | 965395 | 28.2% of identity to the Escherichia coli GTP-binding protein Era; putative | L47648 | <i>Bacillus subtilis</i> | 778 | 41 |
| ORF908 | 968204 | 966975 | poly(A) polymerase | L47709 | <i>Bacillus subtilis</i> | 383 | 41 |
| ORF909 | 968791 | 968237 | ClpX-like protein | U18229 | <i>Bacillus subtilis</i> | 340 | 39 |
| ORF910 | 969498 | 968731 | ATP-dependent protease ATPase subunit | D64006 | <i>Synechocystis sp.</i> | 846 | 66 |
| ORF911 | 969858 | 969511 | ClpP | U16135 | <i>Synechococcus sp.</i> | 257 | 54 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|---------|---------|---|----------|--|-------|----|
| ORF912 | 970118 | 969762 | ATP-dependent clp protease proteolytic component (clpP) | AE000591 | <i>Helicobacter pylori</i> | 362 | 63 |
| ORF913 | 970593 | 970300 | putative | | | | |
| ORF914 | 971261 | 970542 | putative | | | | |
| ORF915 | 971680 | 971123 | putative | | | | |
| ORF916 | 971876 | 975100 | SNF | X98455 | <i>Bacillus cereus</i> | 778 | 49 |
| ORF917 | 975419 | 976516 | MrB protein | M96343 | <i>Bacillus subtilis</i> | 960 | 55 |
| ORF918 | 976584 | 978320 | phospho enol pyruvate carboxykinase | S56812 | <i>Chlorobium limicola</i> | 1667 | 64 |
| ORF919 | 977680 | 977231 | putative | | | | |
| ORF920 | 978399 | 980738 | putative | | | | |
| ORF921 | 980756 | 981928 | putative | | | | |
| ORF922 | 982974 | 981931 | precursor protein (AA -22 to 371) | X52557 | <i>Chlamydia trachomatis</i> | 97 | 50 |
| ORF923 | 984120 | 983119 | NAD+ dependent glycerol-3-phosphate dehydrogenase | L47648 | <i>Bacillus subtilis</i> | 618 | 43 |
| ORF924 | 985502 | 984120 | AgX-1 antigen [human, infertile patient, testis, Peptide, 505 aa] | S73498 | <i>Homo sapiens</i> | 254 | 34 |
| ORF925 | 987180 | 985882 | ORF 4 | M72718 | <i>Bacillus subtilis</i> | 697 | 38 |
| ORF926 | 987172 | 987444 | putative | | | | |
| ORF927 | 989846 | 989049 | nifU-like protein | AE000542 | <i>Helicobacter pylori</i> | 302 | 31 |
| ORF928 | 991048 | 989846 | putative | | | | |
| ORF929 | 991638 | 990955 | phosphoglyceromutase | L09651 | <i>Zymomonas mobilis</i> | 471 | 53 |
| ORF930 | 991794 | 992498 | ORFX13 | L09228 | <i>Bacillus subtilis</i> | 403 | 39 |
| ORF931 | 993619 | 993041 | biotin [acetyl-CoA-carboxylase] ligase | L47709 | <i>Bacillus subtilis</i> | 136 | 38 |
| ORF932 | 993530 | 994792 | rod-shape-determining protein | M22857 | <i>Escherichia coli</i> | 312 | 44 |
| ORF933 | 995970 | 994795 | cadmium-transporting ATPase | D64005 | <i>Synechocystis sp.</i> | 358 | 47 |
| ORF934 | 996857 | 995739 | ATPase | L28104 | <i>Transposon Tn5422</i> | 449 | 39 |
| ORF935 | 997603 | 996782 | putative | | | | |
| ORF936 | 998969 | 997572 | seryl-trna synthetase | Y09924 | <i>Staphylococcus aureus</i> | 851 | 42 |
| ORF937 | 998896 | 1000023 | orf2, homologue to B.subtilis ribG | X64395 | <i>Escherichia coli</i> | 596 | 40 |
| ORF938 | 1000087 | 1001340 | GTP cyclohydrolase II | D90912 | <i>Synechocystis sp.</i> | 1078 | 52 |
| ORF939 | 1001357 | 1001818 | riboflavin synthase beta subunit | U27202 | <i>Actinobacillus pleuropneumoniae</i> | 278 | 36 |
| ORF940 | 1003288 | 1001873 | putative | | | | |
| ORF941 | 1003487 | 1004146 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|---------|---------|--|----------|-----------------------------------|-------|----|
| ORF942 | 1004485 | 1005639 | D-alanine glycine permease (dagA) | AE000603 | <i>Helicobacter pylori</i> | 394 | 33 |
| ORF943 | 1005643 | 1005972 | hypothetical protein MTCY180.08 | Z97193 | <i>Mycobacterium tuberculosis</i> | 274 | 58 |
| ORF944 | 1006784 | 1006116 | similar to trithorax protein in final three exons | U13875 | <i>Caenorhabditis elegans</i> | 155 | 46 |
| ORF945 | 1007563 | 1006769 | ycvJ | D78193 | <i>Bacillus subtilis</i> | 406 | 38 |
| ORF946 | 1009226 | 1007568 | YtpT | AF008220 | <i>Bacillus subtilis</i> | 992 | 47 |
| ORF947 | 1009989 | 1009336 | putative | | | | |
| ORF948 | 1015852 | 1016337 | putative | | | | |
| ORF949 | 1016561 | 1016181 | putative | | | | |
| ORF950 | 1016297 | 1017532 | putative | | | | |
| ORF951 | 1016802 | 1016452 | putative | | | | |
| ORF952 | 1018993 | 1017701 | phenolhydroxylase component | | | | |
| ORF953 | 1019454 | 1019137 | ORF | U32702 | <i>Haemophilus influenzae</i> | 909 | 47 |
| ORF954 | 1020764 | 1019562 | pCTHm1 gene product | M63939 | <i>Escherichia coli</i> | 96 | 45 |
| ORF955 | 1021405 | 1021037 | histone H1-like protein | M94254 | <i>Chlamydia trachomatis</i> | 1185 | 65 |
| ORF956 | 1021821 | 1024286 | phosphoprotein | M80324 | <i>Chlamydia psittaci</i> | 319 | 62 |
| ORF957 | 1024697 | 1024248 | putative | L25078 | <i>Chlamydia trachomatis</i> | 739 | 41 |
| ORF958 | 1025569 | 1024508 | protoporphyrinogen oxidase | U25114 | <i>Mus musculus</i> | 86 | 38 |
| ORF959 | 1026969 | 1025590 | oxygen independent coprophorphyrinogen III oxidase | D90912 | <i>Synechocystis sp.</i> | 880 | 42 |
| ORF960 | 1027789 | 1026947 | uroporphyrinogen decarboxylase | M97208 | <i>Bacillus subtilis</i> | 372 | 38 |
| ORF961 | 1031199 | 1027945 | transcription-repair coupling factor (trcF) (mfd) | U32805 | <i>Haemophilus influenzae</i> | 1584 | 42 |
| ORF962 | 1031717 | 1031172 | alanyl-tRNA synthetase | X95571 | <i>Thiobacillus ferrooxidans</i> | 76 | 31 |
| ORF963 | 1033057 | 1031612 | alanyl-tRNA synthetase | AE000353 | <i>Escherichia coli</i> | 889 | 40 |
| ORF964 | 1033425 | 1033039 | alanyl-tRNA synthetase (alaS) | AE000629 | <i>Helicobacter pylori</i> | 327 | 51 |
| ORF965 | 1033784 | 1033200 | alanyl-tRNA synthetase | X59956 | <i>Rhizobium leguminosarum</i> | 416 | 47 |
| ORF966 | 1033963 | 1036038 | transketolase | Z73234 | <i>Bacillus subtilis</i> | 1398 | 44 |
| ORF967 | 1036945 | 1036010 | AMP nucleosidase | AE000290 | <i>Escherichia coli</i> | 265 | 42 |
| ORF968 | 1037110 | 1037679 | elongation factor P | U14003 | <i>Escherichia coli</i> | 458 | 51 |
| ORF969 | 1037696 | 1037944 | putative | | | | |
| ORF970 | 1038916 | 1037975 | putative | | | | |
| ORF971 | 1040582 | 1039026 | HSP60 chaperonin | X62914 | <i>Clostridium perfringens</i> | 284 | 31 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|--------|---------|---------|---|----------|-----------------------------------|-------|----|
| ORF972 | 1040997 | 1042337 | PROBABLE UDP-N-ACETYL-MURAMOYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15) | AB001488 | <i>Bacillus subtilis</i> | 446 | 39 |
| ORF973 | 1042357 | 1043403 | ORF-Y (AA 1-360) | X51584 | <i>Escherichia coli</i> | 582 | 45 |
| ORF974 | 1043367 | 1044623 | UDP-N-acetylmuramoylalanine-D-glutamate ligase (murD) | U32793 | <i>Haemophilus influenzae</i> | 348 | 42 |
| ORF975 | 1044607 | 1045362 | hypothetical protein | Y14079 | <i>Bacillus subtilis</i> | 115 | 38 |
| ORF976 | 1045384 | 1046538 | spoVE gene product (AA 1-366) | X51419 | <i>Bacillus subtilis</i> | 479 | 35 |
| ORF977 | 1046447 | 1047517 | mur | Y13922 | <i>Enterococcus hirae</i> | 256 | 45 |
| ORF978 | 1047521 | 1049956 | UDP-N-acetylmuramate-alanine ligase (murC) | U32794 | <i>Haemophilus influenzae</i> | 756 | 38 |
| ORF979 | 1050611 | 1050036 | unknown | Z74024 | <i>Mycobacterium tuberculosis</i> | 78 | 44 |
| ORF980 | 1050925 | 1050566 | cycY gene product | U14003 | <i>Escherichia coli</i> | 179 | 34 |
| ORF981 | 1051728 | 1051090 | putative | | | | |
| ORF982 | 1051743 | 1052063 | hypothetical protein | D90908 | <i>Synechocystis sp.</i> | 135 | 33 |
| ORF983 | 1052101 | 1053126 | trna delta(2)-isopentenylpyrophosphate transferase | Z98209 | <i>Mycobacterium tuberculosis</i> | 441 | 37 |
| ORF984 | 1054201 | 1053107 | conserved hypothetical protein | AE000579 | <i>Helicobacter pylori</i> | 826 | 44 |
| ORF985 | 1054242 | 1055555 | putative | | | | |
| ORF986 | 1055483 | 1055908 | putative | | | | |
| ORF987 | 1056609 | 1056965 | YqeL | D84432 | <i>Bacillus subtilis</i> | 202 | 38 |
| ORF988 | 1056961 | 1058232 | beta-ketoacyl-ACP synthase | L13242 | <i>Ricinus communis</i> | 1266 | 55 |
| ORF989 | 1058238 | 1058687 | diadenosine tetraphosphatase | U30313 | <i>Homo sapiens</i> | 122 | 42 |
| ORF990 | 1059371 | 1058727 | inorganic pyrophosphatase (ppa) | AE000576 | <i>Helicobacter pylori</i> | 209 | 39 |
| ORF991 | 1059526 | 1060578 | leucine dehydrogenase LeuDH | U51099 | <i>Bacillus cereus</i> | 680 | 45 |
| ORF992 | 1061553 | 1060579 | 3'(2'),5'-bisphosphate nucleotidase | U40433 | <i>Arabidopsis thaliana</i> | 335 | 43 |
| ORF993 | 1061674 | 1062411 | putative | | | | |
| ORF994 | 1062377 | 1064077 | 2-acylglycerophosphoethanolamine acyl transferase/acyl carrier protein synthetase | U29581 | <i>Escherichia coli</i> | 383 | 44 |
| ORF995 | 1064116 | 1065243 | 7-keto-8-aminopelargonic acid synthetase (bioF) | M29291 | <i>Bacillus sphaericus</i> | 200 | 35 |
| ORF996 | 1067451 | 1065178 | priA | Y10304 | <i>Bacillus subtilis</i> | 1009 | 43 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|--|----------|-----------------------------------|-------|----|
| ORF997 | 1068065 | 1067376 | putative | | | | |
| ORF998 | 1068209 | 1068706 | putative | | | | |
| ORF999 | 1069958 | 1068819 | unknown | U41759 | <i>Chlamydia psittaci</i> | 777 | 41 |
| ORF1000 | 1071163 | 1070033 | unknown | U41759 | <i>Chlamydia psittaci</i> | 381 | 36 |
| ORF1001 | 1072438 | 1071332 | unknown | U41759 | <i>Chlamydia psittaci</i> | 254 | 37 |
| ORF1002 | 1072997 | 1073476 | putative | | | | |
| ORF1003 | 1074239 | 1075864 | lysyl-tRNA synthetase | D90906 | <i>Synechocystis sp.</i> | 1007 | 48 |
| ORF1004 | 1076790 | 1075867 | cysteinyI-tRNA synthetase | L14580 | <i>Bacillus subtilis</i> | 395 | 52 |
| ORF1005 | 1077268 | 1076573 | cys-tRNA synthetase (cysS) | U32693 | <i>Haemophilus influenzae</i> | 431 | 56 |
| ORF1006 | 1077999 | 1078724 | putative | | | | |
| ORF1007 | 1079088 | 1078672 | ribonuclease P protein component (gfg start codon) | M11056 | <i>Escherichia coli</i> | 78 | 46 |
| ORF1008 | 1079642 | 1079944 | 30S ribosomal subunit protein S14 | U18997 | <i>Escherichia coli</i> | 260 | 50 |
| ORF1009 | 1080501 | 1079995 | F18C12.2 | Z75536 | <i>Caenorhabditis elegans</i> | 118 | 38 |
| ORF1010 | 1080775 | 1081341 | putative | | | | |
| ORF1011 | 1083158 | 1081350 | deoxyribodipyrimidine photolyase | J03294 | <i>Bacillus subtilis</i> | 687 | 44 |
| ORF1012 | 1084677 | 1083235 | DNA mismatch repair protein | U71154 | <i>Aquifex pyrophilus</i> | 735 | 48 |
| ORF1013 | 1085648 | 1084632 | DNA mismatch repair protein | D90909 | <i>Synechocystis sp.</i> | 565 | 39 |
| ORF1014 | 1086117 | 1086737 | DNA primase (dnaG) | U32735 | <i>Haemophilus influenzae</i> | 303 | 40 |
| ORF1015 | 1086692 | 1087897 | DnaG | Z83860 | <i>Mycobacterium tuberculosis</i> | 222 | 37 |
| ORF1016 | 1088646 | 1089005 | putative | | | | |
| ORF1017 | 1089146 | 1089805 | putative | | | | |
| ORF1018 | 1092931 | 1089890 | glycyl-tRNA synthetase | U20547 | <i>Chlamydia trachomatis</i> | 2569 | 48 |
| ORF1019 | 1093179 | 1092889 | putative | | | | |
| ORF1020 | 1093584 | 1094204 | phosphatidylglycerophosphate synthase | U87792 | <i>Bacillus subtilis</i> | 163 | 55 |
| ORF1021 | 1095619 | 1094192 | glycogen (starch) synthase | D90899 | <i>Synechocystis sp.</i> | 574 | 40 |
| ORF1022 | 1096074 | 1096628 | partial ctc gene product (AA 1-186) | X16518 | <i>Bacillus subtilis</i> | 86 | 37 |
| ORF1023 | 1096633 | 1097082 | peptidyl-tRNA hydrolase | U31570 | <i>Chlamydia trachomatis</i> | 378 | 53 |
| ORF1024 | 1097266 | 1097601 | ribosomal protein S6 (rps6) | AE000630 | <i>Helicobacter pylori</i> | 179 | 39 |
| ORF1025 | 1097622 | 1097867 | ribosomal protein S18 homolog; putative | M62820 | <i>Chlamydia trachomatis</i> | 324 | 86 |
| ORF1026 | 1097886 | 1098392 | putative heat shock protein ORF; putative | M62820 | <i>Chlamydia trachomatis</i> | 190 | 79 |
| ORF1027 | 1099521 | 1099279 | putative | | | | |
| ORF1028 | 1099689 | 1101053 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | 1% |
|---------|---------|---------|--|----------|---------------------------------------|-------|----|
| ORF1029 | 1102192 | 1101107 | putative | | | | |
| ORF1030 | 1104950 | 1102116 | glycerol-3-phosphate acyltransferase | M80571 | <i>Cucumis sativus</i> | 574 | 43 |
| ORF1031 | 1106508 | 1104946 | ORF_f495; orf of ECMRED, uses 2nd start | U18997 | <i>Escherichia coli</i> | 855 | 38 |
| ORF1032 | 1106722 | 1107249 | putative | | | | |
| ORF1033 | 1107463 | 1108101 | PlsX | U59433 | <i>Bacillus subtilis</i> | 282 | 45 |
| ORF1034 | 1108041 | 1108421 | fatty acid/phospholipid synthesis protein (plsX) | AE000540 | <i>Helicobacter pylori</i> | 205 | 35 |
| ORF1035 | 1108520 | 1113370 | putative 98 kDa outer membrane protein | U72499 | <i>Chlamydia psittaci</i> | 352 | 44 |
| ORF1036 | 1114958 | 1113447 | putative | | | | |
| ORF1037 | 1116915 | 1115071 | lipid A disaccharide synthetase (lpxB) | U32786 | <i>Haemophilus influenzae</i> | 477 | 42 |
| ORF1038 | 1118183 | 1116894 | poly(A) polymerase | AE000123 | <i>Escherichia coli</i> | 555 | 46 |
| ORF1039 | 1118846 | 1120030 | putative | L12968 | <i>Escherichia coli</i> | 880 | 50 |
| ORF1040 | 1120040 | 1120522 | glucosamine fructose-6-phosphate aminotransferase (isomerizing) (glmS) | AE000651 | <i>Helicobacter pylori</i> | 396 | 52 |
| ORF1041 | 1120510 | 1121430 | glutamine amidotransferase; glucosamine--fructose-6-phosphate aminotransferase | AE000450 | <i>Escherichia coli</i> | 494 | 44 |
| ORF1042 | 1121321 | 1121866 | L-glutamine:D-fructose-6-P | U17352 | <i>Thermus aquaticus thermophilus</i> | 374 | 50 |
| ORF1043 | 1122123 | 1122899 | amidotransferase precursor | AE000284 | <i>Escherichia coli</i> | 281 | 41 |
| ORF1044 | 1124842 | 1125564 | tyrosine-specific transport protein | | | | |
| ORF1045 | 1126526 | 1125579 | putative | | | | |
| ORF1046 | 1126519 | 1127676 | cell division protein (ftsY) | U32760 | <i>Haemophilus influenzae</i> | 497 | 41 |
| ORF1047 | 1127672 | 1128571 | succinyl-CoA synthetase beta-subunit | J01619 | <i>Escherichia coli</i> | 784 | 43 |
| | | | succinyl coenzyme A synthetase alpha subunit | U23408 | <i>Dictyostelium discoideum</i> | 978 | 63 |
| ORF1048 | 1130230 | 1131336 | putative | | | | |
| ORF1049 | 1131480 | 1132553 | putative | | | | |
| ORF1050 | 1132830 | 1133843 | putative | | | | |
| ORF1051 | 1134121 | 1134855 | serine protease HtrA | D90905 | <i>Synechocystis sp.</i> | 307 | 51 |
| ORF1052 | 1134642 | 1135592 | GsrA protein | D78376 | <i>Yersinia enterocolitica</i> | 497 | 41 |
| ORF1053 | 1135964 | 1135653 | putative | | | | |
| ORF1054 | 1137132 | 1135954 | R11H6.1 | Z93386 | <i>Caenorhabditis elegans</i> | 445 | 37 |
| ORF1055 | 1137169 | 1140102 | Ydr430cp; CAI: 0.15 | U33007 | <i>Saccharomyces cerevisiae</i> | 559 | 40 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|--|----------|------------------------------------|-------|----|
| ORF1056 | 1141365 | 1140112 | hypothetical 54.7 kD protein in udp 3' region precursor (o475) | AE000459 | <i>Escherichia coli</i> | 222 | 34 |
| ORF1057 | 1142150 | 1141356 | phosphatidylserine synthase (pssA) | AE000614 | <i>Helicobacter pylori</i> | 307 | 41 |
| ORF1058 | 1142520 | 1145660 | ribonucleotide reductase subunit M1 | K02927 | <i>Mus musculus</i> | 1433 | 45 |
| ORF1059 | 1145627 | 1146721 | ribonucleoside diphosphate reductase, beta subunit (nrdB) | AE000553 | <i>Helicobacter pylori</i> | 443 | 32 |
| ORF1060 | 1146862 | 1147545 | unknown | Z95398 | <i>Mycobacterium leprae</i> | 191 | 35 |
| ORF1061 | 1147666 | 1148190 | YtqB | AF008220 | <i>Bacillus subtilis</i> | 262 | 44 |
| ORF1062 | 1148514 | 1148224 | ORF2 | U01958 | <i>Bacillus licheniformis</i> | 135 | 54 |
| ORF1063 | 1149136 | 1148348 | ORF2 | M31827 | <i>Bacillus subtilis</i> | 268 | 40 |
| ORF1064 | 1149702 | 1149166 | putative | | | | |
| ORF1065 | 1150031 | 1150591 | unknown | Z85982 | <i>Mycobacterium tuberculosis</i> | 445 | 49 |
| ORF1066 | 1150785 | 1151147 | ribosomal protein L20 (AA 1-119) | X16188 | <i>Bacillus stearothermophilus</i> | 273 | 44 |
| ORF1067 | 1151165 | 1152181 | phenylalany-tRNA synthetase beta subunit | Z75208 | <i>Bacillus subtilis</i> | 777 | 40 |
| ORF1068 | 1152522 | 1154591 | putative | | | | |
| ORF1069 | 1155666 | 1154566 | putative | | | | |
| ORF1070 | 1156743 | 1155670 | putative | | | | |
| ORF1071 | 1156859 | 1157815 | hypothetical | U32723 | <i>Haemophilus influenzae</i> | 252 | 42 |
| ORF1072 | 1157982 | 1160735 | ATP-binding protein | U01376 | <i>Escherichia coli</i> | 1314 | 56 |
| ORF1073 | 1162620 | 1160917 | polynucleotide phosphorylase | AF010578 | <i>Pisum sativum</i> | 1416 | 52 |
| ORF1074 | 1162970 | 1162590 | polynucleotide phosphorylase | U52048 | <i>Spinacia oleracea</i> | 312 | 53 |
| ORF1075 | 1163532 | 1164020 | orf150 gene product | X95938 | <i>Porphyromonas gingivalis</i> | 335 | 43 |
| ORF1076 | 1163995 | 1164294 | putative | | | | |
| ORF1077 | 1165569 | 1165030 | putative | | | | |
| ORF1078 | 1166108 | 1165566 | putative | | | | |
| ORF1079 | 1166644 | 1166141 | putative | | | | |
| ORF1080 | 1167055 | 1168374 | putative | | | | |
| ORF1081 | 1169218 | 1168337 | methionine aminopeptidase | D64003 | <i>Synechocystis sp.</i> | 488 | 54 |
| ORF1082 | 1169823 | 1169218 | ORF o197 | U18997 | <i>Escherichia coli</i> | 281 | 30 |
| ORF1083 | 1171324 | 1170572 | putative | | | | |
| ORF1084 | 1172085 | 1171177 | hypothetical | U32720 | <i>Haemophilus influenzae</i> | 162 | 44 |
| ORF1085 | 1172394 | 1173773 | fumarase | D64000 | <i>Synechocystis sp.</i> | 1292 | 57 |
| ORF1086 | 1175209 | 1173881 | prs-associated putative membrane protein | U02424 | <i>Escherichia coli</i> | 570 | 39 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|--|----------|-----------------------------------|-------|----|
| ORF1087 | 1175555 | 1175127 | hypothetical protein in pth-prs intergenic region | AE000219 | <i>Escherichia coli</i> | 278 | 46 |
| ORF1088 | 1175778 | 1177043 | hypothetical protein | Z96072 | <i>Mycobacterium tuberculosis</i> | 109 | 43 |
| ORF1089 | 1177177 | 1179048 | putative | | | | |
| ORF1090 | 1179156 | 1180085 | penicillin tolerance protein (lytB) | U32781 | <i>Haemophilus influenzae</i> | 731 | 54 |
| ORF1091 | 1180045 | 1180779 | putative | | | | |
| ORF1092 | 1181942 | 1180788 | putative | | | | |
| ORF1093 | 1182296 | 1181961 | putative | | | | |
| ORF1094 | 1183844 | 1182300 | putative | | | | |
| ORF1095 | 1184420 | 1183848 | putative | | | | |
| ORF1096 | 1185382 | 1184366 | putative | | | | |
| ORF1097 | 1185858 | 1185226 | putative | | | | |
| ORF1098 | 1186164 | 1186481 | putative | | | | |
| ORF1099 | 1187386 | 1186484 | site-specific recombinase | U92524 | <i>Salmonella typhimurium</i> | 401 | 48 |
| ORF1100 | 1187370 | 1189028 | phosphoglucosyltransferase-like protein | L40822 | <i>Chlamydia trachomatis</i> | 1154 | 63 |
| ORF1101 | 1189321 | 1190889 | putative | | | | |
| ORF1102 | 1191142 | 1192146 | NADP-malate dehydrogenase | L40958 | <i>Flavaria bideniis</i> | 775 | 46 |
| ORF1103 | 1191974 | 1191729 | putative | | | | |
| ORF1104 | 1193815 | 1192991 | putative | | | | |
| ORF1105 | 1195702 | 1194248 | α460; This 460 aa orf is 46 pct identical (26 gaps) to 458 residues of an approx. 488 aa protein ARCD PSEAE SW: P18275 | AE000256 | <i>Escherichia coli</i> | 1022 | 44 |
| ORF1106 | 1196303 | 1195716 | putative | | | | |
| ORF1107 | 1196831 | 1196337 | putative | | | | |
| ORF1108 | 1197807 | 1196746 | putative | | | | |
| ORF1109 | 1198740 | 1197883 | putative | | | | |
| ORF1110 | 1200232 | 1198721 | shikimate 5-dehydrogenase | U67551 | <i>Methanococcus jannaschii</i> | 245 | 37 |
| ORF1111 | 1201286 | 1200135 | 3-dehydroquinate synthase (aroB) | U32705 | <i>Haemophilus influenzae</i> | 478 | 45 |
| ORF1112 | 1202386 | 1201259 | 2,3-dihydroxybenzoic acid | L29562 | <i>Vibrio anguillarum</i> | 780 | 50 |
| ORF1113 | 1202901 | 1202350 | putative | | | | |
| ORF1114 | 1204162 | 1202816 | 5-enolpyruvylshikimate 3-phosphate synthase | U67500 | <i>Methanococcus jannaschii</i> | 520 | 40 |
| ORF1115 | 1203177 | 1203464 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|---------------------------------------|----------|--|-------|----|
| ORF1116 | 1205028 | 1204180 | putative | | | | |
| ORF1117 | 1206392 | 1204878 | bioA gene product | A02587 | unidentified | 834 | 48 |
| ORF1118 | 1206742 | 1206086 | dethiobiotin synthase (bioD) | U32830 | <i>Haemophilus influenzae</i> | 243 | 37 |
| ORF1119 | 1207872 | 1206724 | L-alanine - pimelyl CoA ligase | U51868 | <i>Bacillus subtilis</i> | 601 | 41 |
| ORF1120 | 1208852 | 1207851 | biotin synthase | U24147 | <i>Arabidopsis thaliana</i> | 892 | 52 |
| ORF1121 | 1210518 | 1209742 | tryptophan hydroxylase | U26428 | <i>Gallus gallus</i> | 237 | 34 |
| ORF1122 | 1210703 | 1211494 | dihydrodipicolinate reductase | U47017 | <i>Pseudomonas syringae pv. tabaci</i> | 345 | 37 |
| ORF1123 | 1211870 | 1212754 | aspartate-semialdehyde dehydrogenase | U67476 | <i>Methanococcus jannaschii</i> | 444 | 43 |
| ORF1124 | 1212742 | 1214064 | aspartokinase III | U00006 | <i>Escherichia coli</i> | 473 | 47 |
| ORF1125 | 1214046 | 1214858 | dihydrodipicolinate synthase | D64006 | <i>Synechocystis sp.</i> | 238 | 40 |
| ORF1126 | 1215551 | 1216318 | putative | | | | |
| ORF1127 | 1216493 | 1216849 | putative | | | | |
| ORF1128 | 1217183 | 1219612 | putative | | | | |
| ORF1129 | 1220068 | 1219673 | putative | | | | |
| ORF1130 | 1219710 | 1220669 | putative | | | | |
| ORF1131 | 1220630 | 1221376 | putative | | | | |
| ORF1132 | 1221645 | 1223681 | unknown | D26185 | <i>Bacillus subtilis</i> | 621 | 43 |
| ORF1133 | 1223894 | 1224988 | putative | | | | |
| ORF1134 | 1225000 | 1225830 | high level kasamycin resistance | D26185 | <i>Bacillus subtilis</i> | 422 | 41 |
| ORF1135 | 1227810 | 1225879 | hypothetical protein | D90903 | <i>Synechocystis sp.</i> | 1129 | 43 |
| ORF1136 | 1226528 | 1226908 | putative | | | | |
| ORF1137 | 1229972 | 1228311 | exonuclease VII, large subunit (xseA) | U32723 | <i>Haemophilus influenzae</i> | 666 | 46 |
| ORF1138 | 47569 | 47018 | Integrase/recombinase | AE001308 | <i>Chlamydia trachomatis</i> | 716 | 72 |
| ORF1139 | 49980 | 49117 | putative | | | | |
| ORF1140 | 53356 | 52898 | putative | | | | |
| ORF1141 | 54477 | 54884 | O-Sialoglycoprotein Endopeptidase | AE001307 | <i>Chlamydia trachomatis</i> | 311 | 51 |
| ORF1142 | 63753 | 63998 | PTS PEP Phosphotransferase | AE001306 | <i>Chlamydia trachomatis</i> | 198 | 61 |
| ORF1143 | 77164 | 77487 | putative | | | | |
| ORF1144 | 79724 | 79302 | Sms Protein | AE001302 | <i>Chlamydia trachomatis</i> | 458 | 57 |
| ORF1145 | 88721 | 88951 | putative | | | | |
| ORF1146 | 94067 | 94429 | putative | | | | |
| ORF1147 | 122832 | 123341 | hypothetical protein | AE001303 | <i>Chlamydia trachomatis</i> | 398 | 61 |
| ORF1148 | 147536 | 147234 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|--------|--------|---------------------------------|----------|------------------------------|-------|----|
| ORF1149 | 15890 | 159346 | S16 Ribosomal Protein | AE001277 | <i>Chlamydia trachomatis</i> | 467 | 78 |
| ORF1150 | 168470 | 168979 | putative | | | | |
| ORF1151 | 169183 | 169452 | putative | | | | |
| ORF1152 | 171785 | 171504 | Cationic Amino Acid Transporter | AE001278 | <i>Chlamydia trachomatis</i> | 262 | 68 |
| ORF1153 | 172518 | 171775 | Cationic Amino Acid Transporter | AE001278 | <i>Chlamydia trachomatis</i> | 533 | 48 |
| ORF1154 | 193599 | 194045 | putative | | | | |
| ORF1155 | 195704 | 196075 | S/T Protein Kinase | AE001288 | <i>Chlamydia trachomatis</i> | 536 | 82 |
| ORF1156 | 210687 | 210145 | KDO-transferase | X80061 | <i>Chlamydia pneumoniae</i> | 856 | 96 |
| ORF1157 | 211100 | 210708 | putative | | | | |
| ORF1158 | 215420 | 215088 | putative | | | | |
| ORF1159 | 217914 | 218246 | putative | | | | |
| ORF1160 | 218925 | 218701 | putative | | | | |
| ORF1161 | 223785 | 223525 | IMP dehydrogenase | U13372 | <i>Borrelia burgdorferi</i> | 270 | 63 |
| ORF1162 | 224271 | 223999 | putative | | | | |
| ORF1163 | 228691 | 228407 | putative | | | | |
| ORF1164 | 235050 | 235334 | (Methylase) | AE001287 | <i>Chlamydia trachomatis</i> | 331 | 66 |
| ORF1165 | 252308 | 253021 | Oligopeptide Permease | AE001293 | <i>Chlamydia trachomatis</i> | 838 | 72 |
| ORF1166 | 258280 | 258912 | Dicarboxylate Translocator | AE001294 | <i>Chlamydia trachomatis</i> | 909 | 80 |
| ORF1167 | 261325 | 261567 | putative | | | | |
| ORF1168 | 268195 | 268878 | hypothetical protein | AE001287 | <i>Chlamydia trachomatis</i> | 556 | 52 |
| ORF1169 | 269447 | 268881 | putative | | | | |
| ORF1170 | 271263 | 271538 | putative | | | | |
| ORF1171 | 271957 | 272346 | putative | | | | |
| ORF1172 | 274176 | 274550 | putative | | | | |
| ORF1173 | 275736 | 275314 | Disulfide bond Oxidoreductase | AE001291 | <i>Chlamydia trachomatis</i> | 519 | 73 |
| ORF1174 | 276490 | 276927 | hypothetical protein | AE001291 | <i>Chlamydia trachomatis</i> | 249 | 53 |
| ORF1175 | 277577 | 277861 | hypothetical protein | AE001291 | <i>Chlamydia trachomatis</i> | 256 | 52 |
| ORF1176 | 288163 | 287909 | putative | | | | |
| ORF1177 | 290130 | 289789 | putative | | | | |
| ORF1178 | 290989 | 291225 | putative | | | | |
| ORF1179 | 291372 | 291860 | adenylate cyclase | AE001286 | <i>Chlamydia trachomatis</i> | 388 | 48 |
| ORF1180 | 311239 | 311622 | putative | | | | |
| ORF1181 | 328665 | 328384 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|--------|--------|---|----------|------------------------------|-------|----|
| ORF1182 | 337348 | 338289 | sodium-dependent transporter | AF017105 | <i>Chlamydia psittaci</i> | 1112 | 72 |
| ORF1183 | 364764 | 364369 | Prolipoprotein Diacylglycerol Transferase | AE001298 | <i>Chlamydia trachomatis</i> | 300 | 54 |
| ORF1184 | 389623 | 390135 | hypothetical protein | AE001282 | <i>Chlamydia trachomatis</i> | 75 | 33 |
| ORF1185 | 393729 | 394343 | ABC superfamily ATPase | AE001282 | <i>Chlamydia trachomatis</i> | 473 | 52 |
| ORF1186 | 407379 | 407621 | putative | | | | |
| ORF1187 | 410944 | 410708 | putative | | | | |
| ORF1188 | 427632 | 427988 | putative | | | | |
| ORF1189 | 428172 | 428486 | putative | | | | |
| ORF1190 | 436761 | 437246 | hypothetical protein | AE001279 | <i>Chlamydia trachomatis</i> | 661 | 81 |
| ORF1191 | 460911 | 461159 | putative | | | | |
| ORF1192 | 477597 | 477313 | hypothetical protein | AE001300 | <i>Chlamydia trachomatis</i> | 309 | 62 |
| ORF1193 | 487303 | 487001 | putative | | | | |
| ORF1194 | 487764 | 487534 | Glycine Cleavage System H Protein | AE001300 | <i>Chlamydia trachomatis</i> | 221 | 67 |
| ORF1195 | 498502 | 499017 | hypothetical protein | AE001275 | <i>Chlamydia trachomatis</i> | 206 | 32 |
| ORF1196 | 499795 | 500466 | putative | | | | |
| ORF1197 | 571928 | 572344 | putative | | | | |
| ORF1198 | 572367 | 572131 | putative | | | | |
| ORF1199 | 588184 | 587915 | hypothetical protein | AE001312 | <i>Chlamydia trachomatis</i> | 256 | 62 |
| ORF1200 | 600587 | 600907 | (Metalloenzyme) | AE001316 | <i>Chlamydia trachomatis</i> | 314 | 61 |
| ORF1201 | 609731 | 608895 | putative | | | | |
| ORF1202 | 614039 | 614755 | hypothetical protein | AE001317 | <i>Chlamydia trachomatis</i> | 475 | 46 |
| ORF1203 | 614823 | 615152 | putative | | | | |
| ORF1204 | 638244 | 638831 | ABC Transporter ATPase | AE001315 | <i>Chlamydia trachomatis</i> | 614 | 61 |
| ORF1205 | 638819 | 639094 | (Metal Transport Protein) | AE001315 | <i>Chlamydia trachomatis</i> | 265 | 63 |
| ORF1206 | 639073 | 639636 | (Metal Transport Protein) | AE001315 | <i>Chlamydia trachomatis</i> | 687 | 69 |
| ORF1207 | 647901 | 648236 | hypothetical protein | AE001317 | <i>Chlamydia trachomatis</i> | 139 | 38 |
| ORF1208 | 678510 | 679469 | phosphohydrolase | AE001320 | <i>Chlamydia trachomatis</i> | 995 | 63 |
| ORF1209 | 688178 | 688732 | hypothetical protein | AE001320 | <i>Chlamydia trachomatis</i> | 366 | 43 |
| ORF1210 | 696045 | 696563 | methyltransferase | AE001321 | <i>Chlamydia trachomatis</i> | 369 | 49 |
| ORF1211 | 708998 | 708588 | Glucose-1-P Adenylyltransferase | AE001322 | <i>Chlamydia trachomatis</i> | 507 | 83 |
| ORF1212 | 709808 | 710089 | putative | | | | |
| ORF1213 | 718240 | 717737 | Glycerol-3-P Phosphatidyltransferase | AE001323 | <i>Chlamydia trachomatis</i> | 573 | 66 |
| ORF1214 | 737828 | 737565 | S19 Ribosomal Protein | AE001323 | <i>Chlamydia trachomatis</i> | 439 | 94 |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|------------------------------------|----------|------------------------------|-------|----|
| ORF1215 | 779502 | 780257 | hypothetical protein | AE001322 | <i>Chlamydia trachomatis</i> | 476 | 48 |
| ORF1216 | 806310 | 805864 | hypothetical protein | AE001337 | <i>Chlamydia trachomatis</i> | 512 | 67 |
| ORF1217 | 820931 | 820707 | putative | | | | |
| ORF1218 | 837696 | 839096 | Exodeoxyribonuclease V, Gamma | AE001334 | <i>Chlamydia trachomatis</i> | 967 | 49 |
| ORF1219 | 883307 | 883549 | putative | | | | |
| ORF1220 | 892010 | 891726 | putative | | | | |
| ORF1221 | 893277 | 893564 | putative | | | | |
| ORF1222 | 936998 | 937225 | Gen. Secretion Protein E | AE001327 | <i>Chlamydia trachomatis</i> | 256 | 67 |
| ORF1223 | 946865 | 947419 | putative | | | | |
| ORF1224 | 975187 | 975411 | SWF/SNF family helicase | AE001341 | <i>Chlamydia trachomatis</i> | 363 | 96 |
| ORF1225 | 983882 | 985517 | hypothetical protein | AE001342 | <i>Chlamydia trachomatis</i> | 166 | 33 |
| ORF1226 | 987713 | 987180 | hypothetical protein | AE001342 | <i>Chlamydia trachomatis</i> | 447 | 59 |
| ORF1227 | 988215 | 987733 | Flagellar M-Ring Protein | AE001342 | <i>Chlamydia trachomatis</i> | 304 | 44 |
| ORF1228 | 988754 | 988530 | Flagellar M-Ring Protein | AE001342 | <i>Chlamydia trachomatis</i> | 92 | 36 |
| ORF1229 | 992542 | 992841 | hypothetical protein | AE001343 | <i>Chlamydia trachomatis</i> | 112 | 39 |
| ORF1230 | 992759 | 993067 | hypothetical protein | AE001343 | <i>Chlamydia trachomatis</i> | 100 | 32 |
| ORF1231 | 1004247 | 1004528 | D-Ala/Gly Permease | AE001344 | <i>Chlamydia trachomatis</i> | 283 | 64 |
| ORF1232 | 1015013 | 1014294 | 235aa long hypothetical protein | AB009472 | <i>Pyrococcus horikoshii</i> | 104 | 54 |
| ORF1233 | 1056147 | 1056545 | putative | | | | |
| ORF1234 | 1077682 | 1078035 | predicted disulfide bond isomerase | AE001351 | <i>Chlamydia trachomatis</i> | 233 | 46 |
| ORF1235 | 1088121 | 1088381 | putative | | | | |
| ORF1236 | 1098430 | 1098852 | Predicted Kinase | AE001352 | <i>Chlamydia trachomatis</i> | 384 | 59 |
| ORF1237 | 1098798 | 1099319 | Predicted Kinase | AE001352 | <i>Chlamydia trachomatis</i> | 322 | 45 |
| ORF1238 | 1123198 | 1123515 | Transport Permease | AE001354 | <i>Chlamydia trachomatis</i> | 313 | 72 |
| ORF1239 | 1123606 | 1124256 | Tyrosine Transport | AE001354 | <i>Chlamydia trachomatis</i> | 577 | 58 |
| ORF1240 | 1124453 | 1124797 | Tyrosine Transport | AE001354 | <i>Chlamydia trachomatis</i> | 323 | 50 |
| ORF1241 | 1129253 | 1129567 | putative | | | | |
| ORF1242 | 1164947 | 1164474 | hypothetical protein | AE001357 | <i>Chlamydia trachomatis</i> | 412 | 56 |
| ORF1243 | 1170457 | 1170053 | hypothetical protein | AE001358 | <i>Chlamydia trachomatis</i> | 283 | 59 |
| ORF1244 | 1172342 | 1171863 | ABC transporter permease | AE001358 | <i>Chlamydia trachomatis</i> | 457 | 55 |
| ORF1245 | 1192155 | 1192835 | putative | | | | |
| ORF1246 | 1192759 | 1192992 | putative | | | | |
| ORF1247 | 1193861 | 1194142 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|--------------------------------|----------|-----------------------------------|-------|----|
| ORF1248 | 1194036 | 1193779 | (D-Amino Acid Dehydrogenase) | AE001311 | <i>Chlamydia trachomatis</i> | 269 | 79 |
| ORF1249 | 1209748 | 1209053 | conserved hypothetical protein | AE000958 | <i>Archaeoglobus fulgidus</i> | 121 | 38 |
| ORF1250 | 1215111 | 1215419 | putative | | | | |
| ORF1251 | 1216302 | 1216538 | putative | | | | |
| ORF1252 | 1228072 | 1227818 | hypothetical protein | AE001306 | <i>Chlamydia trachomatis</i> | 134 | 39 |
| ORF1253 | 1228304 | 1228080 | xseB | AL021897 | <i>Mycobacterium tuberculosis</i> | 89 | 33 |
| ORF1254 | 26599 | 26222 | putative | | | | |
| ORF1255 | 27609 | 27367 | putative | | | | |
| ORF1256 | 67206 | 66967 | putative | | | | |
| ORF1257 | 70612 | 70352 | putative | | | | |
| ORF1258 | 132703 | 132945 | putative | | | | |
| ORF1259 | 178073 | 178393 | putative | | | | |
| ORF1260 | 208576 | 208349 | putative | | | | |
| ORF1261 | 209156 | 208929 | putative | | | | |
| ORF1262 | 209263 | 209024 | putative | | | | |
| ORF1263 | 210304 | 210639 | putative | | | | |
| ORF1264 | 299009 | 299452 | putative | | | | |
| ORF1265 | 352106 | 351717 | putative | | | | |
| ORF1266 | 420182 | 419949 | Flagellar Secretion Protein | AE001280 | <i>Chlamydia trachomatis</i> | 115 | 43 |
| ORF1267 | 553602 | 553381 | putative | | | | |
| ORF1268 | 556538 | 556807 | putative | | | | |
| ORF1269 | 594348 | 593797 | putative | | | | |
| ORF1270 | 595169 | 594876 | putative | | | | |
| ORF1271 | 662148 | 662381 | putative | | | | |
| ORF1272 | 706528 | 706893 | putative | | | | |
| ORF1273 | 803315 | 803650 | putative | | | | |
| ORF1274 | 849551 | 849306 | putative | | | | |
| ORF1275 | 913676 | 913275 | putative | | | | |
| ORF1276 | 927087 | 926836 | putative | | | | |
| ORF1277 | 930587 | 930360 | putative | | | | |
| ORF1278 | 986531 | 986764 | ORF 12 | M72718 | <i>Bacillus subtilis</i> | 106 | 48 |
| ORF1279 | 996229 | 996486 | putative | | | | |
| ORF1280 | 1000373 | 1000002 | putative | | | | |

| ORF | Begin | End | Homology | ID | Species | Score | I% |
|---------|---------|---------|---------------------------------|----------|------------------------------|-------|----|
| ORF1281 | 1010291 | 1010037 | putative | | | | |
| ORF1282 | 1011128 | 1010793 | 106aa long hypothetical protein | AB009472 | <i>Pyrococcus horikoshii</i> | 159 | 50 |
| ORF1283 | 1012924 | 1012694 | putative | | | | |
| ORF1284 | 1028659 | 1028913 | putative | | | | |
| ORF1285 | 1086481 | 1086762 | putative | | | | |
| ORF1286 | 1118658 | 1118879 | Phosphoglucomutase | AE001354 | <i>Chlamydia trachomatis</i> | 291 | 84 |
| ORF1287 | 1170098 | 1169835 | hypothetical protein | AE001358 | <i>Chlamydia trachomatis</i> | 187 | 53 |
| ORF1288 | 1180828 | 1181184 | putative | | | | |
| ORF1289 | 1182658 | 1183035 | putative | | | | |
| ORF1290 | 1195076 | 1194795 | putative | | | | |
| ORF1291 | 1195890 | 1196183 | putative | | | | |